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l2 and (pro$).ab.	25

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DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=OR			
L7	l2 and (pro$).ab.	25	L7
L6	l1 and ($mg.2).ab.	0	L6
L5	pro-c-mg$	0	L5
L4	"pro-c-mg.2"	0	L4
L3	L2 and (polypep$ OR protein).ab.	37	L3
L2	L1 and (angiogen$).ab.	39	L2
L1	(gerritsen-m$ or goddard-a$ or grimaldi-j$ or mehraban-f$).in.	212	L1

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NEWS 3 Jan 29 FSTA has been reloaded and moves to weekly updates
NEWS 4 Feb 01 DKILIT now produced by FIZ Karlsruhe and has a new update frequency
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NEWS 6 Mar 04 Gene Names now available in BIOSIS
NEWS 7 Mar 22 TOXLIT no longer available
NEWS 8 Mar 22 TSCTHERMO no longer available
NEWS 9 Mar 25 US Provisional Priorities searched with P in CA/CAplus and USPATFULL
NEWS 10 Mar 25 LIPINSKI CALC added for property searching in REGISTRY
NEWS 11 Apr 02 PAPERCHEM no longer available on STN. Use PAPERCHEM2 instead.
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NEWS 16 Apr 22 Records from IP.com available in CAPLUS, HCAPLUS, and ZCAPLUS
NEWS 17 Apr 22 BIOSIS Gene Names now available in TOXCENTER
NEWS 18 Apr 22 Federal Research in Progress (FEDRIP) now available
NEWS 19 Jun 05 New e-mail delivery for search results now available
NEWS 20 Jun 10 MEDLINE Reload
NEWS 21 Jun 10 PCTFULL has been reloaded

NEWS EXPRESS February 1 CURRENT WINDOWS VERSION IS V6.0d, CURRENT MACINTOSH VERSION IS V6.0a(ENG) AND V6.0Ja(JP), AND CURRENT DISCOVER FILE IS DATED 05 FEBRUARY 2002
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  54 FILES SEARCHED...
L1   11 "PRO-C-MG.2"

=> dup rem l1
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L2   10 DUP REM L1 (1 DUPLICATE REMOVED)

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L2   ANSWER 1 OF 10 PROMT COPYRIGHT 2002 Gale Group

ACCESSION NUMBER: 2131:372498 PROMT
TITLE: COMPANY.
SOURCE: Implement & Tractor, (Annual 2001) pp. 4.
                     ISSN: 0019-2953.
PUBLISHER: Freiburg Publishing Co. Inc.
DOCUMENT TYPE: Newsletter
LANGUAGE: English
WORD COUNT: 78063
                     FULL TEXT IS AVAILABLE IN THE ALL FORMAT

L2   ANSWER 2 OF 10 CAPLUS COPYRIGHT 2002 ACS   DUPLICATE 1
AN   2001:266564 CAPLUS
DN   134:291149
TI   Human polypeptides and their corresponding nucleic acids for use in angiogenesis and vascularization
IN   Torrituen, Mary E.; Goddard, Audrey; Grimaldi, J. Christopher; Mehraban, Farl
PA   Genentech, Inc., USA; Curagen Corporation
SO   PCT Int. Appl., 199 pp.
     CODEN: PIXD2
DT   Patent

LA English
FAM.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001025433	A2	20010412	WO 2000-US27511	20001006
	AU 2001084437	A5	20010502		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI US 1999-155587P P 19991007
US 1999-162611P P 19991028

L2 ANSWER 3 OF 10 PROMT COPYRIGHT 2002 Gale Group

ACCESSION NUMBER: 2001:132547 PROMT
TITLE: Manufacturers.
SOURCE: Canadian Machinery and Metalworking, (Dec 2000) Vol. 95, No. 10, pp. 103.
ISSN: 0008-4379.
PUBLISHER: Maclean Hunter Canadian Publishing Ltd.
DOCUMENT TYPE: Newsletter
LANGUAGE: English
WORD COUNT: 64718
FULL TEXT IS AVAILABLE IN THE ALL FORMAT

L2 ANSWER 4 OF 10 PROMT COPYRIGHT 2002 Gale Group

ACCESSION NUMBER: 2001:463252 PROMT
TITLE: COMPANY.(Buyers Guide)
SOURCE: Implement & Tractor, (Annual 2000) pp. 4.
ISSN: 0019-2953.
PUBLISHER: Freiburg Publishing Co. Inc.
DOCUMENT TYPE: Newsletter
LANGUAGE: English
WORD COUNT: 81211
FULL TEXT IS AVAILABLE IN THE ALL FORMAT

L2 ANSWER 5 OF 10 DGENE (C) 2002 THOMSON DERWENT
AN AAE02775 Protein DGENE
TI Polypeptides critical for angiogenesis and vascularization, and the nucleic acids encoding them, useful for treating conditions related to inappropriate vascularization and angiogenesis -
IN Gerritsen M E; Goddard A; Grimaldi J C; Mehraban F
PA (GETH) GENENTECH INC.
(CURA-N) CURAGEN CORP.
PI WO 2001025433 A2 20010412 1[illegible]p
AI WO 2000-US27511 20001006
PRAI US 1999-155587 19991007
US 1999-162611 19991028
DT Patent
LA English
OS 2001-167229 [38]

L2 ANSWER 6 OF 10 DGENE (C) 2002 THOMSON DERWENT

AN AAD[illegible] DNA DGENE
TI Polypeptides critical for angiogenesis and vascularization, and the nucleic acids encoding them, useful for treating conditions related to inappropriate vascularization and angiogenesis -
IN Gerritsen M E; Goddard A; Grimaldi J C; Mehraban F
PA (GETH) GENENTECH INC.
(CURA-N) CURAGEN CORP.
PI WO 200102543[illegible] A2 20010412 189p
AI WO 2000-US27512 20001005
PRAI US 1999-158587 19991007
US 1999-162611 19991028
DT Patent
LA English
OS [illegible]-36722 [38]

L2 ANSWER 7 OF 10 DGENE (C) 2002 THOMSON DERWENT
AN AAD37047 DNA DGENE
TI Polypeptides critical for angiogenesis and vascularization, and the nucleic acids encoding them, useful for treating conditions related to inappropriate vascularization and angiogenesis -
IN Gerritsen M E; Goddard A; Grimaldi J C; Mehraban F
PA (GETH) GENENTECH INC.
(CURA-N) CURAGEN CORP.
PI WO 200102543[illegible] A2 20010412 189p
AI WO 2000-US27512 20001005
PRAI US 1999-158587 19991007
US 1999-162611 19991028
DT Patent
LA English
OS [illegible]-36722 [38]

L2 ANSWER 8 OF 10 DGENE (C) 2002 THOMSON DERWENT
AN AAD37046 DNA DGENE
TI Polypeptides critical for angiogenesis and vascularization, and the nucleic acids encoding them, useful for treating conditions related to inappropriate vascularization and angiogenesis -
IN Gerritsen M E; Goddard A; Grimaldi J C; Mehraban F
PA (GETH) GENENTECH INC.
(CURA-N) CURAGEN CORP.
PI WO 200102543[illegible] A2 20010412 189p
AI WO 2000-US27512 20001005
PRAI US 1999-158587 19991007
US 1999-162611 19991028
DT Patent
LA English
OS [illegible]-36722 [38]

L2 ANSWER 9 OF 10 DGENE (C) 2002 THOMSON DERWENT
AN AAD37045 DNA DGENE
TI Polypeptides critical for angiogenesis and vascularization, and the nucleic acids encoding them, useful for treating conditions related to inappropriate vascularization and angiogenesis -
IN Gerritsen M E; Goddard A; Grimaldi J C; Mehraban F
PA (GETH) GENENTECH INC.
(CURA-N) CURAGEN CORP.
PI WO 200102543[illegible] A2 20010412 189p
AI WO 2000-US27512 20001005
PRAI US 1999-158587 19991007
US 1999-162611 19991028
DT Patent

LA English
OS 2001-367229 [38]

L2 ANSWER 1 OF 10 DGENE (C) 2002 THOMSON DERWENT
AN AAD07043 cDNA DGENE
TI Polypeptides critical for angiogenesis and vascularization, and the nucleic acids encoding them, useful for treating conditions related to inappropriate vascularization and angiogenesis -
IN Gurnitsen M P; Goddard A; Grimaldi J C; Mehraban F
PA (GETH) GENENTECH INC.
    (CURA-N) CURAGEN CORP.
PI WO 2001025433 A2 20010412 16pp
AI WO 2000-US27512 20001005
PRAI US 1999-158587 19991007
    US 1999-162611 19991028
DT Patent
LA English
OS 2001-367229 [38]

OM protein - protein search, using sw model

Run on: [illegible] 2002, 09:57:39 ; Search time 66.81 Seconds
(without alignments)
[illegible] Million cell updates/sec

Title: US-09-684-458-2
Perfect score: [illegible]
Sequence: 1 M[illegible]V[illegible]IV .... [illegible]EAK[illegible]ALERIC 577

Scoring table: BLOSUM62
Gap [illegible] Gapext 0.5

Searched: 105224 seqs, 38713550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: [illegible]
Maximum DB seq length: [illegible]

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Maximum Match 100%
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Database : SwissProt_40:*

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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	[illegible]	[illegible]	968	1	ST10_HUMAN	O94804 homo sapien
2	[illegible]	[illegible]	1081	1	KCK1_YEAST	Q12236 saccharomyc
3	[illegible]	[illegible]	966	1	ST10_MOUSE	O55098 mus musculu
4	[illegible]	5.7	1895	1	YLK3_CAEEL	P41951 caenorhabdi
5	[illegible]	5.6	736	1	KPCE_RABIT	P10830 oryctolagus
6	[illegible]	5.6	737	1	KPCE_HUMAN	Q02156 homo sapien
7	[illegible]	5.5	737	1	KPCE_MOUSE	P16054 mus musculu
8	[illegible]	5.4	[illegible]	1	SNXG_HUMAN	P57768 homo sapien
9	[illegible]	5.3	[illegible]	1	SNXG_RAT	P57769 rattus norv
10	[illegible]	5.3	[illegible]	1	PKPA_PHYBL	Q01577 phycomyces
11	[illegible]	5.2	[illegible]	1	Y537_HUMAN	O60285 homo sapien
12	[illegible]	5.1	737	1	KPCE_RAT	P09216 rattus norv
13	[illegible]	5.1	[illegible]	1	KPC4_DROME	P83099 drosophila
14	[illegible]	5.1	[illegible]	1	CK14_MAIZE	[illegible]24585 zea mays (m
15	[illegible]	5.1	[illegible]	1	SOS2_MOUSE	[illegible]2384 mus musculu
16	[illegible]	5.1	[illegible]	1	SNXD_HUMAN	[illegible]y5w8 homo sapien
17	[illegible]	5.1	1101	1	[illegible]A2_HUMAN	[illegible]60879 homo sapien
18	[illegible]	4.9	[illegible]	1	ERB2_RAT	P06494 rattus norv
19	[illegible]	4.9	[illegible]	1	MSKE_MOUSE	Q9wu16 mus musculu
20	[illegible]	4.8	[illegible]	1	KPCD_HUMAN	[illegible] homo sapien
21	144	4.8	[illegible]	1	ERB2_HUMAN	P04626 homo sapien
22	[illegible]	4.8	[illegible]	1	YAV_[illegible]	Q10172 schizosacch
23	[illegible]	4.8	[illegible]	1	[illegible]_CANAL	[illegible] candida alb
24	[illegible]	4.7	[illegible]	1	ST24_HUMAN	Q9y6e0 homo sapien
25	[illegible]	4.7	[illegible]	1	SPKD_SYNY3	P54735 synechocyst
26	[illegible]	4.7	[illegible]	1	ST[illegible]_CAEEL	P46549 caenorhabdi
27	[illegible]	4.6	743	1	KPC[illegible]_APLCA	Q16975 aplysia cal
28	[illegible]	4.6	426	1	ST25_HUMAN	O00506 homo sapien
29	[illegible]	4.6	[illegible]	1	KPCD_MOUSE	P28867 mus musculu
30	[illegible]	4.6	[illegible]	1	ABL_MLVAB	P00521 abelson mur
31	[illegible]	4.6	[illegible]	1	BNR[illegible]_YEAST	P40450 saccharomyc
32	[illegible]	4.6	842	1	CLA4_YEAST	P48562 saccharomyc
33	[illegible]	4.6	[illegible]	1	SOS2_HUMAN	Q07890 homo sapien
34	137.5	4.6	1490	1	CRK7_HUMAN	Q9nyv4 homo sapien
35	137	4.6	673	1	KPCI_RAT	P09215 rattus norv
36	137	4.6	939	1	ST20_YEAST	Q03497 saccharomyc
37	137	4.6	1254	1	ERB2_MESAU	Q60553 mesocricetu
38	137	4.6	1273	1	MYS3_YEAST	P36006 saccharomyc
39	137	4.6	1567	1	FMN2_MOUSE	Q9jl04 mus musculu
40	136	4.5	369	1	CD5S_MOUSE	[illegible]35926 mus musculu
41	136	4.5	426	1	ST25_MOUSE	Q9z2w1 mus musculu
42	136	4.5	501	1	WASL_RAT	[illegible]08816 rattus norv
43	135.5	4.5	505	1	WASL_BOVIN	Q95107 bos taurus
44	135.5	4.5	634	1	KPC3_DROME	P13678 drosophila
45	134.5	4.5	374	1	SNXE_HUMAN	Q9y5w7 homo sapien

ALIGNMENTS

RESULT 1
ST10_HUMAN
ID   ST10_HUMAN   STANDARD;   PRT;   968 AA.
AC   O94804; Q9U1W4;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Serine/threonine-protein kinase 1[illegible] (EC 2.7.1.-) (Lymphocyte-oriented
DE   kinase).
GN   STK10 OR LOK.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID 9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99216434; PubMed 1019991[illegible];
RA   Kuramochi S., Matsuda Y., Okamoto M., Kitamura [illegible], Yonekawa H.,
RA   Karasuyama H.;
RT   "Molecular cloning of the human gene STK10 encoding lymphocyte-
RT   oriented kinase, and comparative chromosomal mapping of the human,
RT   mouse, and rat homologues.";
RL   Immunogenetics 49:369-375(1999).
RN   [2]
RP   SEQUENCE OF 814-968 FROM N.A.
RC   TISSUE Testis;
RA   Bloecker H., Boecher M., Brandt P., Mewes H. W., Gassenhuber J.,
RA   Wiemann S.;
RL   Submitted (NOV 1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: CAN ACT ON SUBSTRATES SUCH AS MYELIN BASIC PROTEIN AND
CC   HISTONE IIA ON SERINE AND THREONINE RESIDUES (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN LYMPHOID ORGANS.
CC   -!- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   STE20 SUBFAMILY.
CC   --
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CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; AB015718; BAA35073.1; -.
DR   EMBL; AL133081; CAB61400.1; -.
DR   HSSP; P24941; 1HCL.
DR   MIM; 603919; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

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DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Phosphorylation; Coiled coil.
FT   DOMAIN       [illegible]    [illegible]       PROTEIN KINASE.
FT   DOMAIN       573    647       COILED COIL (POTENTIAL).
FT   DOMAIN       [illegible]    884       GLN RICH.
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FT   BINDING      65     65        ATP (BY SIMILARITY).
FT   ACT_SITE     [illegible]    [illegible]       BY SIMILARITY.
SQ   SEQUENCE   968 AA;  112134 MW;  15E2451[illegible] CRC64;

  Query Match             6.6%;  Score 199.5;  DB 1;  Length 968;
  Best Local Similarity   24.2%;  Pred. No. 0.00043;
  Matches  123;  Conservative   60;  Mismatches  184;  Indels  141;  Gaps   25;

Qy        113 EKVKKE[illegible]NNY[illegible]ANY[illegible]VMET[illegible]LEEWEVVELEED[illegible]WR[illegible]EE[illegible]MK[illegible]KNQF 172
Db         24 EHVERELDENEV                        WEIVGELGD-GAFGKVY--KAKN-- 55

Qy        173 KEELVLSWADLGPDKYLSD-KDFQCLIKLLESCLHPYIYRVIFATANESSALLIRMFNEK 231
Db         56 KETGALAAAKVIETKSEEELEDYIVEIEILATCDHPYIVKLLGAYYHDGKLWIMIEFCPG 115

Qy        232 [illegible] 291
Db        116 GAVDAIMLELD          RGLTEPQIQVVCRQMLEALNFLHSKRIIHRDLKA 160

Qy        292 [illegible] 332
Db        161 [illegible]FYWMA   ELVVHE[illegible] 217

Qy        333 VEVHEFGHLLYEMIYGRPP  DSVPV        DSEPP   APSMAVVAVLESILSCEAC 380
Db        218 [illegible]NEMPVLEKIAE[illegible]EWKDVL [illegible]LKIALE 276

Qy        381 KN  [illegible]MPLEGDVELLTSEKPQEK[illegible]ARKEEKEQ[illegible] 438
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Qy        439 Q[illegible]EIEAL[illegible]EEEKPKEIARKEEKEQEALENCEEECARYCNENNSSSGASSPL F 497
Db        320 [illegible]       DEGEEEE        AVDAASILENHIQNSSEVSPPS-  INADKPLEE 360

Qy        498 [illegible]          LSGISALPPPPPPPPPP        AAPLP      PASTEV 534
Db        361 [illegible]SVNEP[illegible]SDRSLQTISEPVVAPQNENGLAVPVPLRKSREVSMDA 420

Qy        535 PALLSSQAVNSMSRGALLSSIQNPQKGI 562
Db        421 KLQVAQEKQVAEQGGGSPAANRSQKAS 448


RESULT 4
KKQ0_YEAST
ID   KKQ0_YEAST     STANDARD;      PRT;  1081 AA.
AC   Q12236;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   [illegible] (Rel. 40, Last annotation update)
DE   Probable serine/threonine-protein kinase YOL100W (EC 2.7.1.-).
GN   YOL100W OR HRC1081.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96076631; PubMed=7502582;
RA   Vandenbol M., Durand P., Portetelle D., Hilger F.;
RT   "Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV
RT   including the Ty1-H3 retrotransposon, the suf1(+) frameshift
RT   suppressor gene for tRNA-Gly, the yeast transfer RNA Thr-1a and a
RT   delta element.";
RL   Yeast 11:1069-1075(1995).
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       PKC SUBFAMILY.
CC   --------------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; Z48149; CAA88162.1; -.
DR   EMBL; Z74842; CAA99113.1; -.
DR   HSSP; P00517; 1STC.
DR   SGD; S0005460; YOL100W.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Hypothetical protein; Transferase; Serine/threonine-protein kinase;
KW   ATP-binding.
FT   DOMAIN       179    443       PROTEIN KINASE.
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FT   BINDING      208    208       ATP (BY SIMILARITY).
FT   ACT_SITE     303    303       BY SIMILARITY.
SQ   SEQUENCE   1081 AA;  121[illegible] MW;  [illegible] CRC64;

  Query Match             6.5%;  Score 195;  DB 1;  Length 1081;
  Best Local Similarity   21.4%;  Pred. No. 0.00087;
  Matches  103;  Conservative   74;  Mismatches  161;  Indels  144;  Gaps   20;

Qy        [illegible] EEYLEKL[illegible]FLVLSWA[illegible]CLHPYIYRVIFATANES 220
Db        202 EEEYAAEV[illegible]NNS-[illegible]PSVV[illegible]EQDES 251

Qy        221 SALLIRMEN[illegible]EIVEEELR 280
Db        252 SLYFLLEYAPNGDFLSLMKKYGSLDETCARY          [illegible]YAAQIIDAIDYLH 295

Qy        281 DKGFPYGHLHASNVMLDGD             [illegible]PEKINILP 331
Db        296 [illegible]SEVGIAE 354

Qy        332 GV                  DVHCPGHLLYEMIYGRPLSVEVP                   [illegible] 365
Db        355 YV[illegible]LEVMKVQYAFIPGPL 414

Qy        366 AVVAVLESILSCEACKN--GMPLISRLLQMPLESDVLL  -        TTSEKPQEKIPIKC 415
Db        415 [illegible]EEYEINAES 470

Qy        416 KEAL------RIAKECI----EERLIEEQK      -QIHQRRELEAQSHRCSEEERKKR 459
Db        471 [illegible]ACTECEICK 530

Qy        460 KILARKKSAKSA--LEN--               -               SEEHSARYSNSN 486
Db        531 K    RPTEERIAQTLENAKKGINNEKNQ[illegible]AA[illegible]AA[illegible]AAL[illegible]KEIMQSYE[illegible] 587

Qy        487 NSGSGASSPLIS--------          -PSSPIPPSISGISALPPPPPPPPPPAAPLPPA 530
Db        588 [illegible]MSEEMITY 647

Qy        531 ST 532
Db        648 DT 649
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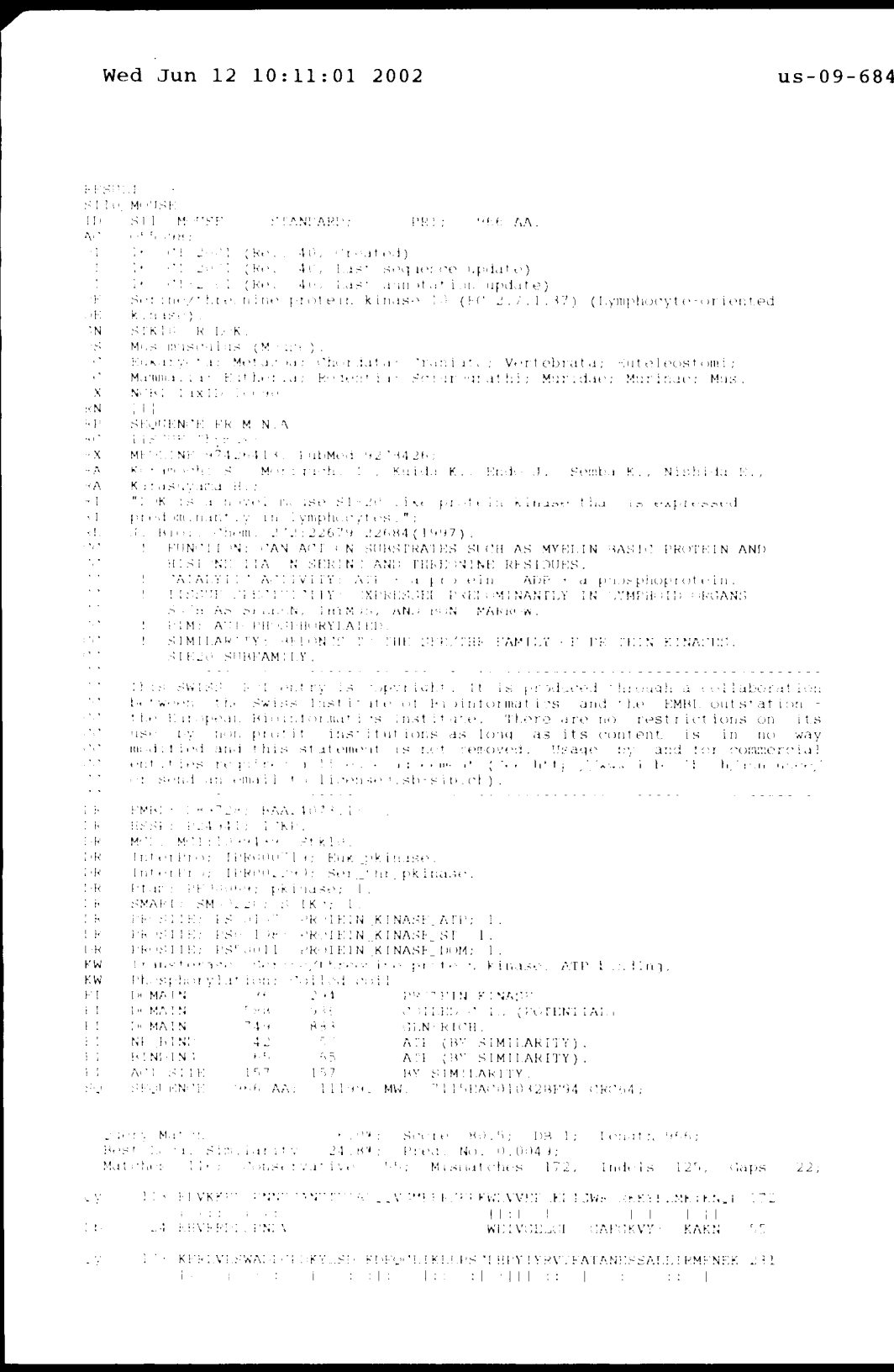

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FT   NP_BIND     4[illegible]    445       ATP (BY SIMILARITY).
FT   BINDING     4[illegible]    4[illegible]       ATP (BY SIMILARITY).
FT   ACT_SITE    5[illegible]    5[illegible]       BY SIMILARITY.
SQ   SEQUENCE   1895 AA;  208[illegible] MW;  E2[illegible]  CRC64;

  Query Match              5.7%;  Score 170.5;  DB 1;  Length 1895;
  Best Local Similarity   21.8%;  Pred. No. 0.041;
  Matches  [illegible];  Conservative   93;  Mismatches  209;  Indels  229;  Gaps   40;

Qy         [illegible] IEVLKII        SVENE        WQIVRPYSDPELLNNSLQIA[illegible]        PLP 76
Db     229 IEIYD[illegible]STENC[illegible]WHVAWILAQLAEQHE[illegible]ISLEIAQ[illegible]EFAAI[illegible]NPKP 285

Qy      77 IKKEIINMSEELIA                    EFLK[illegible]    YL       NVIIINR 107
Db     286 I[illegible]KAVI    [illegible]WVAML[illegible]ALLAQLA[illegible]NANGVYI[illegible]KKNVIIDEF 341

Qy     1[illegible]    LSN[illegible]                         ELVKKELDPNNYQA    NYIEIALQQ 135
Db     342 [illegible]WEI[illegible]EFVEKLMYIFEKSRQLLEKV[illegible]EFVNYNVV[illegible]IAKMY 401

Qy     1[illegible] VDM[illegible]   EKSEEKWEVV             EPEKE[illegible]        WKIKKKYIS[illegible] 172
Db     4[illegible] EN[illegible]EENIEIMKIWEIVNEE[illegible]AV[illegible]VYIVKKK  A[illegible]NE 459

Qy     1[illegible] KEIIVLD     WA[illegible]                        EEVITAIANL[illegible] 227
Db     4[illegible] AEIIALKEEIMINENDRE  SEKSP[illegible]MISEVKI[illegible]LRHPNIVRYREIFV   ENRK[illegible] 514

Qy     2[illegible] [illegible]RMENEK[illegible]YKAKE[illegible]KEY NEKE[illegible]KIY[illegible]ILLEVLKEPL[illegible] 281
Db     515 YIVMEL[illegible]IMKEE   KGNE[illegible]KEIWAMYV         [illegible]NMGALEYLHK[illegible] 5[illegible]2

Qy     2[illegible] K[illegible]PY[illegible]HBAENVMLD[illegible]KELLDLENSLLQL      PSEYRS      YESQEEKINIL  330
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Qy     3[illegible]   [illegible]SVD[illegible]HLYEMIY[illegible]PDSVPVDSEEEAPSMAVVAVLESILSCEACKNGMELIS 388
Db     6[illegible] [illegible]EKA[illegible]WSE[illegible]YEM[illegible]                    VEHST      NMLILAM 652

Qy     3[illegible]   [illegible]M      [illegible]   V[illegible]EKEKA[illegible]AKE[illegible] 4[illegible]9
Db     653 [illegible]QVEAKYI[illegible]LNEMWS[illegible]LEE[illegible]LAPD     ESARPDILKVSQMC[illegible]VELLEYLDDVAR 708

Qy     440 HPK     [illegible]HAQ[illegible]HHQSEEEEKEEE[illegible]LAEEK[illegible]EE[illegible]ALENQLLHGAK[illegible]NN[illegible] 1[illegible]7
Db     7[illegible] [illegible]QLA[illegible]MIA[illegible]YNIKD[illegible]          ESPSSENSSISSYEEP[illegible]SSKIS[illegible]KLPP 758

Qy     4[illegible]            [illegible]SPIEPSEDQISALP          PPPPPPPPPAAPLPPASIEVPAQL 538
Db     759 INPAEPPNHQ[illegible]AGEIPPE[illegible]IVQLPRIIDKYSVMPISAPSAIPSRKKVQ[illegible]SIEHPARS 818

Qy     5[illegible]A    VNEM[illegible]ALLSS 554
Db     8[illegible]   [illegible]KVQK[illegible]VSS 837

RESULT   [illegible]
KPCE_RABIT
ID   KPCE_RABIT     STANDARD;      PRT;   736 AA.
AC   [illegible]
DT   01-[illegible]-19[illegible] (Rel. 1[illegible], Created)
DT   01-[illegible]-19[illegible] (Rel. 1[illegible], Last sequence update)
DT   15-[illegible]-[illegible] (Rel. 39, Last annotation update)
DE   Protein kinase C, epsilon type (EC 2.7.1.[illegible]) (nPKC-epsilon).
GN   PRKCE.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=8822[illegible]; PubMed=3370672;
RA   Ohno S., Akita Y., Konno Y., Imajoh S., Suzuki K.;
RT   "A novel phorbol ester receptor/protein kinase, nPKC, distantly
RT   related to the protein kinase C family.";
RL   Cell 53:731-741(1988).
CC   -!- FUNCTION: THIS IS CALCIUM INDEPENDENT, PHOSPHOLIPID DEPENDENT,
CC       SERINE- AND THREONINE-SPECIFIC ENZYME.
CC   -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC       PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC       THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC   -!- SIMILARITY: CONTAINS 2 ZINC-DEPENDENT PHORBOL ESTER AND DAG
CC       BINDING DOMAINS.
CC   -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       PKC SUBFAMILY.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; M20014; AAA31426.1; -.
DR   PIR; A28963; KIRBCE.
DR   HSSP; P28867; 1PTQ.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR002219; DAG_PE-bind.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF00130; DAG_PE-bind; 2.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00433; pkinase_C; 1.
DR   PRINTS; PR00008; DAGPEDOMAIN.
DR   SMART; SM00109; C1; 2.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
DR   PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR   PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   Repeat; ATP-binding; Transferase; Phosphorylation;
KW   Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
FT   DOMAIN        1     99       C2 DOMAIN.
FT   DOMAIN      170    220       PHORBOL-ESTER AND DAG BINDING 1.
FT   DOMAIN      243    292       PHORBOL-ESTER AND DAG BINDING 2.
FT   DOMAIN      407    667       PROTEIN KINASE.
FT   NP_BIND     413    421       ATP (BY SIMILARITY).
FT   BINDING     436    436       ATP (BY SIMILARITY).
FT   ACT_SITE    531    531       BY SIMILARITY.
FT   MOD_RES     702    702       PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT   MOD_RES     709    709       PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ   SEQUENCE   736 AA;  83515 MW;  261C4FEE59E9BFEB CRC64;

  Query Match              5.6%;  Score 168.5;  DB 1;  Length 736;
  Best Local Similarity   23.2%;  Pred. No. 0.017;
  Matches   76;  Conservative   48;  Mismatches  125;  Indels   79;  Gaps   15;

Qy     1[illegible] KY[illegible]MK[illegible]KEV[illegible]KV[illegible]EYL[illegible]IEV[illegible]TA 217
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Qy     218 NKSFAL[illegible]NKNE[illegible]YKAKPK[illegible]KKY NEKK[illegible]KIYQLLEVLK 2[illegible]
Db     477 TKDRLFFVMEYVNGG    DLMFQIQRS    RKFDEPRS           RFYAAEVISALM 520
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Qy        278 FLHDKGFPYGHLHASNVML[illegible]                ENSL[illegible]LPSFYRSYFSQF 324
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Qy        325 EKINTLESVDVIE[illegible]GHLLYEMIYGHPP                DSVEVDS  [illegible]FLFAPSMAVVAVLE 372
Db        58[illegible]  ELEY[illegible]VDWWAL[illegible]VLMYEMMA[illegible]                VLY[illegible]VW[illegible]KEAVS[illegible]ILK [illegible]

Qy        37[illegible] S           [illegible]TLSCFACKNCMP[illegible]        V[illegible]            KE    417
Db        [illegible] AFMTKNPHKRL[illegible]VAAQN[illegible]AIK    [illegible]WVLLEQRKIEPPFKPRIKSKN [illegible]

Qy        41[illegible]                 [illegible]ALKIAKEF[illegible]EKRLIEEQ 434
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RESULT [illegible]
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ID   KPCE_HUMAN   STANDARD;   PRT;   737 AA.
AC   Q0215[illegible];
DT   [illegible] JUL 1993 (Rel. 2[illegible], Created)
DT   [illegible] JUL 1993 (Rel. 2[illegible], Last sequence update)
DT   15 JUL 1999 (Rel. 3[illegible], Last annotation update)
DE   Protein kinase C, epsilon type (EC 2.7.1.-) (NPKC-epsilon).
GN   PRKCE OR PKCE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93033318; PubMed=1382605;
RA   Basta P., Strickland M.B., Holmes W., Loomis C.R., Ballas L.M.,
RA   Burns D.J.;
RT   "Sequence and expression of human protein kinase C-epsilon.";
RL   Biochim. Biophys. Acta 1132:154-160(1992).
CC   -!- FUNCTION: THIS IS CALCIUM INDEPENDENT, PHOSPHOLIPID DEPENDENT,
CC   SERINE- AND THREONINE-SPECIFIC ENZYME.
CC   -!- [illegible] WHICH IN TURN
CC   PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC   THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC   -!- SIMILARITY: CONTAINS 2 ZINC DEPENDENT PHORBOL ESTER AND DAG
CC   BINDING DOMAINS.
CC   -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC   -!- SIMILARITY: [illegible] FAMILY [illegible]
CC   PKC SUBFAMILY.
CC   --
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CC   modified and this statement is not removed. Usage by and for commercial
CC   [illegible]
CC   or send an email to license@isb-sib.ch).
CC   --
DR   EMBL; X[illegible]; CAA4[illegible].1; -.
DR   PIR; S28[illegible]42; S28[illegible]42.
DR   HSSP; P[illegible]; 1PTQ.
DR   MIM; 1[illegible]; -.
DR   InterPro; IPR00[illegible]; C2.
DR   InterPro; IPR002219; DAG_PE_bind.
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DR   InterPro; IPR00[illegible]; Pkinase_C.
DR   InterPro; IPR00[illegible]; Ser_thr_pkinase.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF00130; DAG_PE_bind; 2.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00433; pkinase_C; 1.
DR   PRINTS; PR00008; DAGPEDOMAIN.
DR   SMART; SM00[illegible]; C2; 1.
DR   SMART; SM00[illegible]; C1; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; [illegible].
DR   PROSITE; PS00479; DAG_PE_BIND_DOMAIN_1; 2.
DR   PROSITE; PS50081; DAG_PE_BIND_DOMAIN_2; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   Repeat; ATP-binding; Transferase; Phosphorylation;
KW   [illegible] protein kinase; Phorbol-ester binding; Zinc.
FT   DOMAIN   1   99   C2 DOMAIN.
FT   [illegible]
FT   DOMAIN   243   292   PHORBOL-ESTER AND DAG BINDING 2.
FT   DOMAIN   408   668   PROTEIN KINASE.
FT   NP_BIND   414   422   ATP (BY SIMILARITY).
FT   BINDING   437   437   ATP (BY SIMILARITY).
FT   ACT_SITE   532   532   BY SIMILARITY.
FT   MOD_RES   703   703   PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT   MOD_RES   710   710   PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ   SEQUENCE   737 AA; 83673 MW; [illegible] CRC64;

Query Match   5.6%; Score 167.[illegible]; DB [illegible]; Length 737;
Best Local Similarity   23.2%; Pred. No. [illegible];
Matches   76; Conservative   48; Mismatches 125; Indels   79; Gaps   15;

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Qy        162 KYFLMKIENQFEERLVLSWAL[illegible]          [illegible]SCIHYIYRVIFATA 217
Db        421 KVMLAELKGKDE   VYAVKVLKKDV[illegible]AKKHPYLIQLY[illegible]FQ 477

Qy        218 NESSAL[illegible]KEY[illegible]N[illegible]FF[illegible]EVIK 277
Db        478 TKDRLFFVMEYVNGG---DLMFQIQRS----RKFDEPRS      ----RFYAAEVTSALM 521

Qy        278 FLHDKGFPYGHLHASNVMLDGD-TCKLLDL-------        ENSLLGLPSFYRSYFSQF 324
Db        522 FLHQHGVIYRDLKLDNILLDAEGH[illegible]KLADFGMCKEGILNGVTTTTFCGTPDYIAPEILQ 580

Qy        325 EKINTLESVDVIEFGHLLYEMIYGHPP   ---     DSVEVDS -FLFAPSMAVVAVLE 372
Db        581 ELEYGPSVDWWALGVLMYEMMAGQPPFEA[illegible]VLYEVWLKKEAVSILK 639

Qy        373 S----------TLSCFACKNCMP[illegible]     VL[illegible]   KE     417
Db        640 AFMTKNPHKRLGCVAAQNGEDAIK[illegible]WVLLEQRKIKPPFKPRIKSKN 696

Qy        418              ALKIAKEFTEKRLIEEQ 434
Db        697 NFDQDFTREEPVLTLVDEAIVKQINQEE 724
```

RESULT 7
KPCE_MOUSE
ID   KPCE_MOUSE   STANDARD;   PRT;   737 AA.
AC   P16054;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Protein kinase C, epsilon type (EC 2.7.1.-) (NPKC-epsilon).
GN   PRKCE OR PKCE OR PKCEA.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89137541; PubMed=2917659;
RA   Schaap D., Parker P.J., Bristol A., Kriz R., Knopf J.;
RT   "Unique substrate specificity and regulatory properties of
RT   PKC-epsilon: a rationale for diversity.";
RL   FEBS Lett. 243:351-357(1989).
RN   [2]
RP   SEQUENCE FROM N.A.

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RC   TISSUE=Brain;
RX   MEDLINE=[illegible]; PubMed=[illegible];
RA   Wang [illegible], Acs P., Goodnight J., Blumberg P.M., Mischak H.,
RA   Mushinski J.F.;
RT   "The catalytic domain of PKC epsilon, in reciprocal PKC delta and -
RT   epsilon chimeras, is responsible for conferring tumorigenicity to
RT   NIH3T3 cells, whereas both regulatory and catalytic domains of
RT   PKC epsilon contribute to in vitro transformation.";
RL   Oncogene 16:53-60(1998).
CC   -!- FUNCTION: THIS IS CALCIUM INDEPENDENT, PHOSPHOLIPID DEPENDENT,
CC       SERINE AND THREONINE SPECIFIC ENZYME.
CC   -!- FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN
CC       PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVES AS
CC       THE RECEPTOR FOR PHORBOL ESTERS, A CLASS OF TUMOR PROMOTERS.
CC   -!- SIMILARITY: CONTAINS 2 ZINC DEPENDENT PHORBOL ESTER AND DAG
CC       BINDING DOMAINS.
CC   -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       PKC SUBFAMILY.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF[illegible]; AAB64[illegible].1; -.
DR   PIR; [illegible]; KIMSCE.
DR   HSSP; [illegible]; [illegible].
DR   MGD; MGI:[illegible]; Pkce.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR002219; DAG PE bind.
DR   InterPro; IPR000719; Euk pkinase.
DR   InterPro; IPR000961; Pkinase C.
DR   InterPro; IPR002290; Ser thr pkinase.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF00130; DAG PE bind; 2.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00433; pkinase C; 1.
DR   PRINTS; PR00008; DAGPEDOMAIN.
DR   SMART; SM00109; C1; 2.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM00133; S TK X; 1.
DR   SMART; SM00220; S TKc; 1.
DR   PROSITE; PS50004; C2 DOMAIN 2; 1.
DR   PROSITE; PS00479; DAG PE BIND DOM 1; 2.
DR   PROSITE; PS50081; DAG PE BIND DOM 2; 2.
DR   PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR   PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR   PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW   Repeat; ATP-binding; Transferase; Phosphorylation;
KW   Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
FT   DOMAIN        [illegible]   [illegible]   C2 DOMAIN.
FT   DOMAIN        [illegible]   [illegible]   PHORBOL ESTER AND DAG BINDING 1.
FT   DOMAIN        24[illegible] [illegible]   PHORBOL ESTER AND DAG BINDING 2.
FT   DOMAIN        4[illegible]  [illegible]   PROTEIN KINASE.
FT   NP_BIND       434    442       ATP (BY SIMILARITY).
FT   BINDING       4[illegible]  4[illegible]  ATP (BY SIMILARITY).
FT   ACT_SITE      [illegible]   [illegible]   BY SIMILARITY.
FT   MOD_RES       [illegible]   [illegible]   PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT   MOD_RES       [illegible]   [illegible]   PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ   SEQUENCE   737 AA;  [illegible] MW;  7AEBB0[illegible]0[illegible]9E57 CRC64;

  Query Match             5.5%;  Score 166.5;  DB 1;  Length 737;
  Best Local Similarity   23.2%;  Pred. No. 0.022;
  Matches  [illegible];  Conservative  [illegible];  Mismatches  125;  Indels  79;  Gaps  15;

Qy        [illegible] KYEEMKIEN[illegible]KE[illegible]VLSWA[illegible]DEY[illegible]SD[illegible]SLK  [illegible]VTKVIFAIA 217
Db        [illegible] KVHLAEL[illegible]KD  VYAVKVLKK[illegible]VIL[illegible]DDV[illegible]CHMTEKRILALAK[illegible]YL[illegible] 477

Qy        218 NSEA[illegible]IEMLNEKCSLEKLLYRAKTR[illegible]LKKY[illegible]NEKKL[illegible]LEEQ[illegible]KIEY[illegible]GQLLEVLE 277
Db        478 TKDRLFFVMEYVNGG---DLMFQIQRS     RKFDEPRS          RFYAAEVISALM 521

Qy        278 FLHEKGFYYCHLHASNVMLDQD TCKLLD             ENCLLQLEETYEFEYESQF 324
Db        522 FLHQHGVIYRDLKLDNILLDAEGHCKLADFGMCKEGIMNGVTTTTFCGTPDYIAPEILQ 580

Qy        325 EKINI[illegible]LVDVHGGHLLYEMIYGRE[illegible]       DSVEVEG LEEALSMAVVAVLE 372
Db        581 ELEYGPSVDWWALGVLMYEMMAGQPPFEADNEDDLFESILHDDVLYPVWLSKEAVSILK 639

Qy        373 E          [illegible]CPACKNCMPE[illegible]ELLQHPEIFSD  VLLPIST KPQEKIPIKLKE    417
Db        640 AFMTKNPHKRLGCVAAQNGEDAIK---QHPFFKEIDWVLLEQKKIKPPFKPRIKTKRDVN 696

Qy        418             ALKIAEEPTIEKLIEEQ 434
Db        697 NFDQDFTREEPILTLVDEAIIKQINQEE 724


RESULT 8
SNX16_HUMAN
ID   SNX16_HUMAN     STANDARD;      PRT;   343 AA.
AC   P57768;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Sorting nexin 16.
GN   SNX16.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hanson B.J., Hong W.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: MAY BE INVOLVED IN SEVERAL STAGES OF INTRACELLULAR
CC       TRAFFICKING.
CC   -!- SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY.
CC   -!- SIMILARITY: CONTAINS 1 PHOX HOMOLOGY (PX) DOMAIN.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; AF305779; AAG25676.1; -.
DR   InterPro; IPR001683; PX.
DR   Pfam; PF00787; PX; 1.
DR   SMART; SM00312; PX; 1.
KW   Transport; Protein transport; Coiled coil.
FT   DOMAIN       110    211       PX.
FT   DOMAIN       224    278       COILED COIL (POTENTIAL).
SQ   SEQUENCE   343 AA;  39153 MW;  EBE7722[illegible]BA46FF5 CRC64;

  Query Match             5.4%;  Score 161.5;  DB 1;  Length 343;
  Best Local Similarity   29.0%;  Pred. No. 0.016;
  Matches   51;  Conservative   29;  Mismatches   74;  Indels   [illegible];  Gaps   [illegible];

Qy         17 IVFLIAAIEAGQSLQGHIEYIIEVQRGIGVENGWQIVRRYSDFDLLNNSLQ  IAGLSLP 74
Db        108 SIPTILGYEVMEERAKFTVYKILVEK  [illegible]WVVFRRYTEFYRLNDKLKEMFPGFRLA 16[illegible]

Qy         75 LLEKKL[illegible]NK[illegible]EFIAERQKGLQNYLNVLIN[illegible]SLN[illegible]LVKEFL  [illegible]NNYSANYIE 1[illegible]
Db        [illegible] LL[illegible]KKWEK[illegible]S[illegible]NA[illegible]LL[illegible]KEQ[illegible]LQAEL[illegible]NLVA[illegible]LA[illegible]ANCLAVKEFLCLDD[illegible]      [illegible]
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Qy    [illegible] IA[illegible]VSMFFR[illegible]FWFVV[illegible]FKYFLMFIKNQFEERLV[illegible]WAFLCPL 186
Db    [illegible]                FEFDS[illegible]SEA[illegible]IN[illegible]LEEQKEM[illegible]LKK[illegible]KQ[illegible] 2[illegible]

RESULT [illegible]
SNXG_RAT
ID   SNXG_RAT       STANDARD;      PRT;   344 AA.
AC   [illegible]
DT   [illegible]-OCT-2001 (Rel. 40, Created)
DT   [illegible]-OCT-2001 (Rel. 40, Last sequence update)
DT   [illegible]-OCT-2001 (Rel. 40, Last annotation update)
DE   Sorting nexin [illegible]
GN   SNX[illegible].
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=[illegible];
RN   [1]
RP   SEQUENCE FROM N.A.
RA   [illegible] W.;
RL   Submitted (SEP-[illegible]) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: MAY BE INVOLVED IN SEVERAL STAGES OF INTRACELLULAR
CC       TRAFFICKING.
CC   -!- SIMILARITY: BELONGS TO THE SORTING NEXIN FAMILY.
CC   -!- SIMILARITY: CONTAINS 1 PHOX HOMOLOGY (PX) DOMAIN.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF[illegible]; AAG[illegible]; -.
DR   InterPro; IPR001683; PX.
DR   Pfam; PF[illegible]; [illegible]
DR   Pfam; PF[illegible]; PX; 1.
DR   SMART; SM00312; PX.
KW   Transport; Protein transport; Coiled coil.
FT   DOMAIN      [illegible]    [illegible]       PX.
FT   DOMAIN      [illegible]    278       COILED COIL (POTENTIAL).
SQ   SEQUENCE   344 AA;  [illegible] MW;  E7A[illegible]C2[illegible]022F CRC64;

  Query Match             5.[illegible]%;  Score 158.5;  DB 1;  Length 344;
  Best Local Similarity   3[illegible]%;  Pred. No. 0.024;
  Matches   [illegible];  Conservative   27;  Mismatches   62;  Indels   17;  Gaps    6;

Qy    [illegible] IVF[illegible]
Db    [illegible]8 SIP[illegible]CYEVMFEFAKFIVYF[illegible]VFF--[illegible]FEFWVVFFRYT[illegible]FLN[illegible]KEMF[illegible]A 1[illegible]5

Qy    [illegible] LFEKK[illegible]NM[illegible]IAEL[illegible]NYINVT[illegible]NH[illegible]KEL   [illegible] 1[illegible]
Db    1[illegible]6 LFFKFWKEFNYNA[illegible]FLFDF[illegible]LQAFLQNLVAHE[illegible]ANCIAVKEFL[illegible]LE 225

Qy    1[illegible]5 SANV[illegible]KWVV[illegible] 1[illegible]5
Db    226 SKA[illegible]LEEINYH[illegible]EEEKQKEV[illegible]KEL 2[illegible]7

RESULT [illegible]
PKPA_PHYBL
ID   PKPA_PHYBL     STANDARD;      PRT;   613 AA.
AC   Q[illegible];
DT   15-[illegible]-199[illegible] (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   [illegible]-OCT-2001 (Rel. 40, Last annotation update)
DE   Serine/threonine protein kinase PKPA (EC 2.7.1.-).
GN   PKPA.
OS   Phycomyces blakesleeanus.
OC   Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
OC   Phycomyces.
OX   NCBI_TaxID=4837;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NRRL 1555;
RX   MEDLINE=96120859; PubMed=859047[illegible];
RA   Ruiz Perez V.L., Murillo F.J., Torres Martinez S.;
RT   "PkpA, a novel Phycomyces blakesleeanus serine/threonine protein
RT   kinase.";
RL   Curr. Genet. 28:309-316(1995).
CC   -!- FUNCTION: SERINE/THREONINE PROTEIN KINASE THAT MAY EARLY
CC       PARTICIPATES AS AN INTERMEDIATE IN AN INTRACELLULAR SYSTEM
CC       CONTROLLING NUCLEAR PROLIFERATION.
CC   -!- DEVELOPMENTAL STAGE: MAINLY EXPRESSED DURING THE VEGETATIVE
CC       GROWTH. THE LEVEL DECREASED WHEN THE MYCELIUM CAN DIFFERENTIATE
CC       AND FORM SPORANGIOPHORES.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
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CC   --------------------------------------------------------------------------
DR   EMBL; Z46636; CAA86606.1; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE NEG.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding.
FT   DOMAIN       17    269       PROTEIN KINASE.
FT   NP_BIND      23     31       ATP (BY SIMILARITY).
FT   BINDING      50     50       ATP (BY SIMILARITY).
FT   ACT_SITE    140    140       BY SIMILARITY.
SQ   SEQUENCE   613 AA;  69594 MW;  [illegible] CRC64;

  Query Match             5.3%;  Score [illegible];  DB [illegible];  Length 613;
  Best Local Similarity   20.9%;  Pred. No. [illegible];
  Matches   99;  Conservative   65;  Mismatches  [illegible];  Indels  120;  Gaps   1[illegible];

Qy    192 KLF[illegible]LIKLL[illegible]LHFTIYKVIFA[illegible]  NE[illegible]ALL[illegible]KMFNEK[illegible]LIYKAKIKLPFLK 249
Db     57 KDLGHEIDILKSVKHPNI   ITFHDAWYNEIFVFITFLM[illegible]GILFEYIKKLTPLP       110

Qy    [illegible]
Db    111              NIKIVKKW[illegible]QILK[illegible]LAYLH[illegible]HE[illegible]IHR[illegible]KPNIFINGAHGEIKIGD 159

Qy    [illegible]4 [illegible]LLEN[illegible]SLLSLL[illegible]YKGYF[illegible]IKK[illegible]VF[illegible]QHLIYFSFYGRPP      [illegible]1
Db    160 MCTAEMKNGKKYTVIGTPEFMAPEMYEEQ[illegible]YN  EKV[illegible]YALGM[illegible]LEMAIGEYPYGECT 217

Qy    [illegible]2 [illegible]                        [illegible]FVFV[illegible]FFPAF[illegible]MAVVAVLE[illegible]CEACKNEM [illegible]84
Db    218 NAVQVFKKVIQ[illegible]IKPECLSRVQDPE[illegible]LVNI[illegible]FEPEEM[illegible]AQ[illegible]LESHRF[illegible]  AVEFEV 275

Qy    385 PIISRLLQMPLFS-DVLLTISEK- [illegible]KII[illegible]KLKFAL[illegible]IAKD[illegible]IEKK[illegible]IFFQK[illegible] 43[illegible]
Db    276 VLVS[illegible]KDMT[illegible]KL[illegible]LQVVI[illegible]KGMEKL[illegible]VK[illegible]NA[illegible]AA[illegible]VVALMI[illegible]VI[illegible]N[illegible]YQQLITC 335

Qy    438 HQHRRLTRAQSHHGSEEERKKKK[illegible]LAKKKSK-KSALENS  ---------  475
Db    336 EINK[illegible]RD[illegible]ARNQGPPDKGEEEKIVWKK[illegible]NI[illegible]KSEIKKAKK[illegible]LALAVEKVFEAKKKGELL 395

Qy    476 EDHG     ARYGNGNN[illegible]GACT[illegible]PPPEPPPAAP      526
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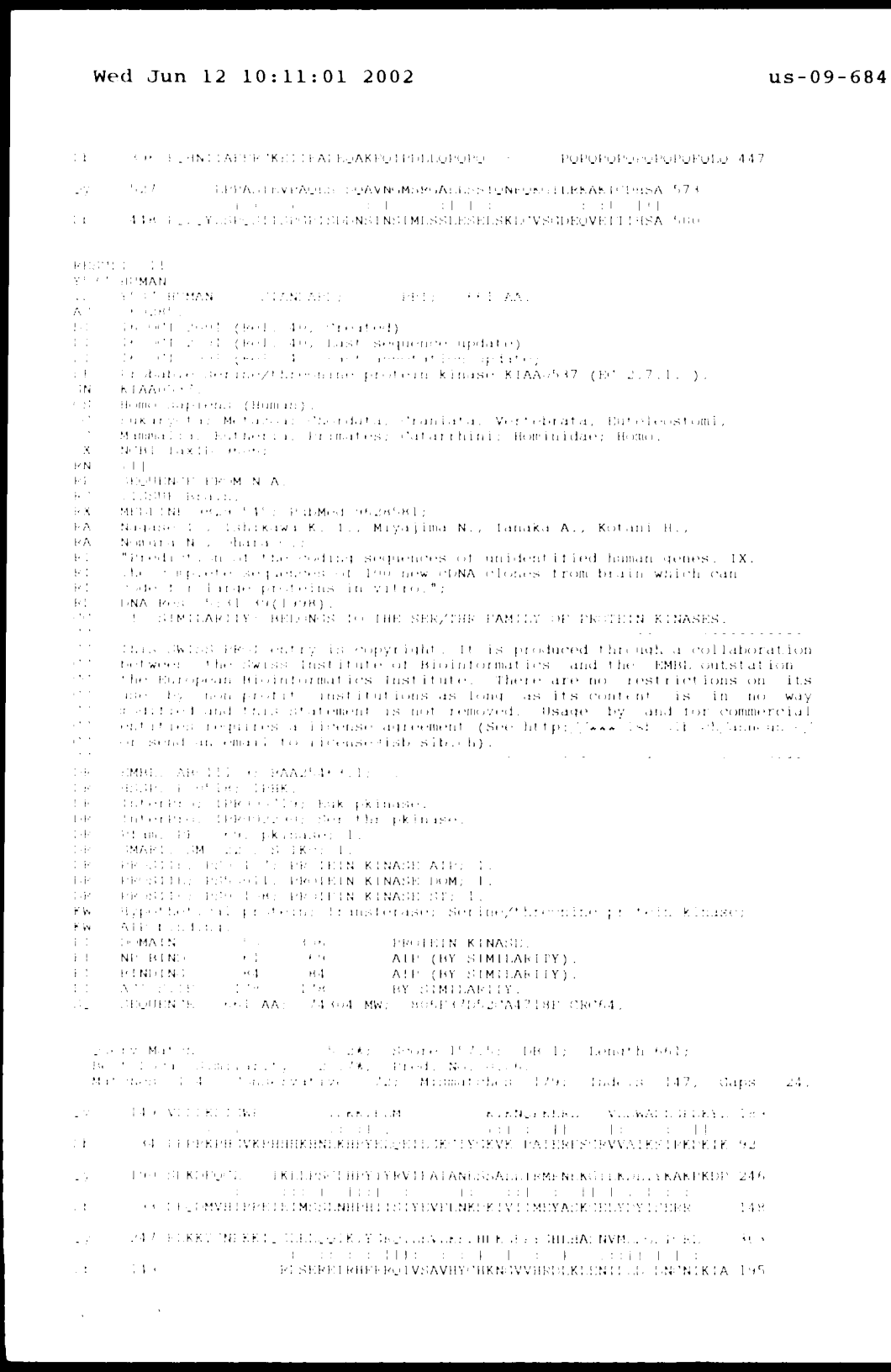

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DR   EMBL; M18[illegible]; AAA41872.1; -.
DR   PIR; [illegible]; KIR[illegible].
DR   HSSP; [illegible]; 1PTQ.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR002219; DAG_PE-bind.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF00130; DAG_PE-bind; 2.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00433; pkinase_C; 1.
DR   PRINTS; [illegible]; DAG [illegible]MAIN.
DR   SMART; SM[illegible]; C1; 2.
DR   SMART; SM00239; C2; 1.
DR   SMART; SM[illegible]; S_TK_X;
DR   SMART; SM[illegible]; [illegible]; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
DR   PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DR   PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   Repeat; ATP-binding; Transferase; Phosphorylation;
KW   Serine/threonine-protein kinase; Phorbol-ester binding; Zinc.
FT   DOMAIN        1     90       C2 DOMAIN.
FT   DOMAIN       [illegible]    220      PHORBOL-ESTER AND DAG BINDING 1.
FT   DOMAIN      213    292      PHORBOL-ESTER AND DAG BINDING 2.
FT   DOMAIN      [illegible]    [illegible]      PROTEIN KINASE.
FT   NP_BIND     414    4[illegible]      ATP (BY SIMILARITY).
FT   BINDING     [illegible]    4[illegible]      ATP (BY SIMILARITY).
FT   ACT_SITE    [illegible]    [illegible]      BY SIMILARITY.
FT   MOD_RES     [illegible]    [illegible]      PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT   MOD_RES     [illegible]    [illegible]      PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ   SEQUENCE   [illegible] AA;  [illegible] MW;  [illegible] CRC64;

  Query Match             5.1%;  Score 15[illegible]5;  DB 1[illegible];  Length 737;
  Best Local Similarity   22.9%;  Pred. No. 0.12;
  Matches  [illegible];  Conservative   47;  Mismatches  127;  Indels   79;  Gaps   15;

Qy        1[illegible] K[illegible]VMEIKN[illegible]VL[illegible]EYL[illegible]K[illegible]CLIE     LLFS[illegible]LEYIYEVIFATA 217
Db        4[illegible]1 KVMLAE[illegible]K[illegible]DE  -VYAVKVLKK[illegible]VI[illegible]VD[illegible]IMIEKRILALARK[illegible]PYL[illegible]QLY[illegible]FQ 177

Qy        2[illegible] N[illegible]MPN[illegible]EPLIYEAKE[illegible]LKEY[illegible]NPEKI[illegible]QIKTYGRQILIVLK 277
Db        4[illegible] [illegible]KLFFVMEYVNG[illegible]MFQ[illegible]RS-   [illegible]KEDEPKS---------GFYAAEVTSALM 521

Qy        2[illegible] FIH[illegible]K[illegible]Y[illegible]HI[illegible]ASNVMI[illegible]RLL[illegible]-------------[illegible]NS[illegible]P[illegible]FYRSYP[illegible]QP 324
Db        5[illegible] FLH[illegible]GVIYRDLKL[illegible]NILL[illegible]A[illegible]GHSKLA[illegible]GM[illegible]NGV[illegible]TF[illegible]CG[illegible]PDYIAPEILQ- 580

Qy        [illegible] [illegible]KINIIE[illegible]VI[illegible]VH[illegible]HLLYEMIYGRPP          DSVPVDS- FPPAPSMAVVAVLE 372
Db        5[illegible] [illegible]                                                 [illegible]KLAV[illegible]LK 63[illegible]

Qy        37[illegible] S    [illegible]  [illegible]LS[illegible]PA[illegible]                 [illegible]     41[illegible]
Db        640 [illegible]WV[illegible]KEMK[illegible]KIEKPVN 696

Qy        41[illegible]            -ALKIAKECIEKRLIEDQ 434
Db        [illegible] NP[illegible]VPEAIVKQINQEF [illegible]

RESULT [illegible]
KPC4_DROME
ID   KPC4_DROME     STANDARD;      PRT;   5[illegible] AA.
AC   [illegible]VYN[illegible];
DT   01-MAR-2002 (Rel. 41, Created)
DT   01-MAR-2002 (Rel. 41, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Putative protein kinase C, delta type homolog (EC 2.7.1.-) (Fragment).
GN   Pkcdelta or CG10524.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=1073[illegible];
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., [illegible], [illegible] K.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., [illegible], Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   CONCEPTUAL TRANSLATION.
RA   Manning G., Sudarsanam S., Plowman G.;
RT   "Prediction of novel protein kinases from the Drosophila genome
RT   project and EST sequences.";
RL   Unpublished observations (AUG-2[illegible]).
CC   -!- SIMILARITY: CONTAINS 2 ZINC [illegible] PHORBOL-ESTER AND DAG
CC       BINDING DOMAINS.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       PKC SUBFAMILY.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; AE003489; AAF48163.1; ALT_SEQ.
DR   FlyBase; FBgn0039387; Pkcdelta.
DR   HSSP; P28867; 1PTQ.
DR   InterPro; IPR002219; DAG_PE-bind.
DR   InterPro; IPR000719; Euk_pkinase.
```

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DE   Inferit ; IPR000961; PKinase_C.
DE   Inferit ; IPR002290 ; Ser/Thr pkinase.
DE   Inferit ; IPR003245; Tyr pkinase.
DE   Pfam; PF00069; DAG_PE-bind; 2.
DE   Pfam; PF00069; pkinase; 1.
DE   Pfam; PF00433; pkinase_C; 2.
DE   PRINTS; PR00008; DAGPEDOMAIN.
DE   PRINTS; PR00109; TYRKINASE.
DE   SMART; SM00109; C1; 2.
DE   SMART; SM00220; S_TKc; 1.
DE   SMART; SM00233; STYKc; 1.
DE   SMART; SM00219; TyrKc; 1.
DE   PROSITE; PS00479; DAG_PE_BIND_DOM_1; 2.
DE   PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
DE   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DE   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DE   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   Hypothetical protein; ATP-binding; Transferase;
KW   Serine/threonine protein kinase; Phorbol ester binding; Metal-binding;
KW   Zinc; Repeat.
FT   NP_BIND       :       :
FT   DOMAIN        65      95          PHORBOL ESTER/DAG BINDING 1.
FT   DOMAIN        97      147         PHORBOL ESTER/DAG BINDING 2.
FT   DOMAIN        159     444         PROTEIN KINASE.
FT   NP_BIND       165     240         ATP (BY SIMILARITY).
FT   BINDING       225     225         ATP (BY SIMILARITY).
FT   ACT_SITE      341     341         BY SIMILARITY.
SQ   SEQUENCE   514 AA;  59422 MW;  99E9C96D62AA497E CRC64;


  Query Match             5.1%;  Score 154;  DB 1;  Length 514;
  Best Local Similarity  24.5%;  Pred. No. 0.006;
  Matches  96;  Conservative  37;  Mismatches  124;  Indels   70;  Gaps   13;

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

RESULT 14
Q11 MAIZ
ID   Q11 MAIZ     STANDARD;      PRT;   901 AA.
AC   Q24560;
DT   01-DEC-1998 (Rel. 37, Created)
DT   01-DEC-1998 (Rel. 37, Last sequence update)
DT   xx-MAY-2000 (Rel. xx, Last annotation update)
DE   Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.1. ).
GN   CR4
OS   Zea mays (Maize).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC   Panicoideae; Andropogoneae; Zea.
OX   NCBI_TaxID=4577;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. B73;
RX   MEDLINE=96455669; PubMed=8723079;
RA   Becraft P.W., Stinard P.S., McCarty D.R.;
RT   "CRINKLY4: A TNFR-like receptor kinase involved in maize epidermal
RT   differentiation.";
RL   Science 273:1406-1409(1996).
CC   -!- FUNCTION: PUTATIVE RECEPTOR PROTEIN KINASE. COULD PLAY A ROLE IN A
CC       DIFFERENTIATION SIGNAL. THE CRINKLY4 (CR4) MUTATION AFFECTS LEAF
CC       EPIDERMIS DIFFERENTIATION SUCH THAT CELL SIZE AND MORPHOLOGY ARE
CC       ALTERED, AND SURFACE FUNCTIONS ARE COMPROMISED, ALLOWING GRAFT
CC       LIKE FUSIONS BETWEEN ORGANS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC   -!- SIMILARITY: CONTAINS A PARTIAL LA NGFR/TNFR TYPE CYSTEINE-RICH
CC       REGION.
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CC   -----------------------------------------------------------------------
DR   EMBL; U67422; AAB09771.1; -.
DR   MaizeDB; 128723; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR003245; STY_pkinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001368; TNFR_c6.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00020; TNFR_c6; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00208; TNFR; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR   PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.
DR   PROSITE; PS50050; TNFR_NGFR_2; 1.
KW   Receptor; Transferase; Serine/threonine protein kinase; ATP-binding;
KW   Repeat; Transmembrane; Signal.
FT   SIGNAL      1     24          POTENTIAL.
FT   CHAIN       25    901         PUTATIVE RECEPTOR PROTEIN KINASE
FT                                 CRINKLY4.
FT   DOMAIN      25    423         EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    424   444         POTENTIAL.
FT   DOMAIN      445   901         CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      33    330         7 X 36 AA REPEATS.
FT   REPEAT      33    68          1.
FT   REPEAT      72    107         2.
FT   REPEAT      125   160         3.
FT   REPEAT      162   195         4.
FT   REPEAT      203   236         5.
FT   REPEAT      254   287         6.
FT   REPEAT      292   330         7.
FT   REPEAT      357   391         TNFR-CYS.
FT   DOMAIN      569   712         PROTEIN KINASE.
FT   NP_BIND     511   519         ATP (BY SIMILARITY).
FT   BINDING     533   533         ATP (BY SIMILARITY).
FT   ACT_SITE    634   634         BY SIMILARITY.
SQ   SEQUENCE   901 AA;  97439 MW;  52F8481AC187E061 CRC64;


  Query Match             5.1%;  Score 154;  DB 1;  Length 901;
  Best Local Similarity  20.1%;  Pred. No. 0.2%;
  Matches  104;  Conservative  89;  Mismatches  192;  Indels  132;  Gaps   22;

Qy      [illegible]
Db      [illegible]
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Qy    [illegible] [illegible]VSMFFKSE[illegible]KWFVV[illegible] ---------- [illegible]EEKYIIMEIKN 170
Db    [illegible] LAKSIAYSEKK[illegible]NMK[illegible]KIRRA[illegible]FFSYEEL[illegible]QAICCFSEDS[illegible]VCKQSPSCVPKC 522

Qy    [illegible] [illegible]IKFEIVLS[illegible]KY[illegible]IKILF[illegible]LHIYIYKVIIPATANESGALLIRMF 228
Db    [illegible] [illegible]VVAVK[illegible]VKK[illegible]FHNEL[illegible]LSRLNHAHLLNL[illegible]SERLIVYEP 582

Qy    [illegible] NFK[illegible] 285
Db    [illegible] MAH[illegible]HLH [illegible]KKE[illegible]NWAFKV [illegible]AVQAA[illegible]YLHGYACIIV [illegible]

Qy    286 YGHIHASNVM[illegible]DLENSLIGL[illegible] DSFYRSYFSQF 324
Db    [illegible] IHRDIKSSNILLD[illegible]INARVADFGLSIIGPADSGTPLSE[illegible]PAGTLQYLDPEYYRLHYI-- 688

Qy    325 RKINILESVLVE[illegible]LLYEMIYGRPPLSVPVD------SFFPAFSMAVVAVLESILS 376
Db    [illegible] [illegible]IKSLVYSF[illegible]VVLLEILSGRKAIDMQFEEGNIVEWAVPLIKAGDIFAILDPVLSP 743

Qy    [illegible] [illegible] 420
Db    744 FSLIEA[illegible]VAN[illegible]VEM [illegible]EVT[illegible]ALEEAL[illegible]LMQSP[illegible] 795

Qy    421 [illegible]RA[illegible]SHH[illegible]SEPPEKK--- ------- - - EKILAPKKSKRSA 471
Db    796 [illegible]EVVL[illegible]SSPMHKVSQMG[illegible]NHSTSENL[illegible]APGI[illegible]YRAPSW[illegible]TIL[illegible]SVIISQRKKSSA 855

Qy    472 LENS[illegible]FSARYSN[illegible]NNG[illegible]GGPLIG [illegible] 502
Db    856 SE[illegible]APIV[illegible]FRAI[illegible]RNV[illegible]SS[illegible]LESLPEFIAPASP 891


RESULT [illegible]
S[illegible]S2_MOUSE
ID   S[illegible]S2_MOUSE     STANDARD;     PRT;  1297 AA.
AC   [illegible]
DT   15-[illegible]-[illegible] (Rel. [illegible], Created)
DT   [illegible] (Rel. [illegible], Last sequence update)
DT   [illegible] MAR-2002 (Rel. 41, Last annotation update)
DE   Son of sevenless protein homolog 2 (SOS-2) ([illegible]) (Fragment).
GN   SOS2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; [illegible]; Muridae; Murinae; Mus.
OX   NCBI_TaxID=[illegible];
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SWISS [illegible];
RX   MEDLINE=[illegible]; PubMed=[illegible]5);
RA   Bowtell D.D., Fu [illegible], Simon M.A., [illegible] P.V.;
RT   "Identification of murine homologues of the Drosophila son of
RT   sevenless gene: potential activators of ras.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:6511-6515(1992).
CC   -!- FUNCTION: PROMOTES THE EXCHANGE OF RAS BOUND GDP BY GTP (BY
CC       SIMILARITY).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN MOST EMBRYONIC AND ADULT TISSUES.
CC   -!- SIMILARITY: CONTAINS 1 DBL HOMOLOGY DOMAIN (DH).
CC   -!- SIMILARITY: CONTAINS [illegible] PH DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 RASGEF DOMAIN.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; [illegible]; AAA[illegible].
DR   PIR; S25714; S25714.
DR   HSSP; [illegible]; 1PMS.
DR   MGD; MGI:[illegible]; Sos2.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR000651; RasGEFN.
DR   InterPro; IPR001895; RasGRF_CDC25.
DR   InterPro; IPR000219; RhoGEF.
DR   Pfam; PF00169; PH; 1.
DR   Pfam; PF00617; RasGEF; 1.
DR   Pfam; PF00618; RasGEFN; 1.
DR   Pfam; PF00621; RhoGEF; 1.
DR   SMART; SM00233; PH; 1.
DR   SMART; SM00147; RasGEF; 1.
DR   SMART; SM00229; RasGEFN; 1.
DR   SMART; SM00325; RhoGEF; 1.
DR   PROSITE; PS00741; DH_1; FALSE_NEG.
DR   PROSITE; PS50010; DH_2; 1.
DR   PROSITE; PS00720; GDS_CDC25; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
KW   Guanine nucleotide releasing factor.
FT   NON_TER       1      1
FT   DOMAIN      164    353       DH.
FT   DOMAIN      407    510       PH.
FT   DOMAIN      740    926       RASGEF.
FT   DOMAIN     1145   1148       POLY-PRO.
FT   DOMAIN     1154   1173       POLY-PRO.
SQ   SEQUENCE   1297 AA;  148846 MW;  [illegible] CRC64;

  Query Match             5.1%;  Score [illegible];  DB [illegible];  Length 1297;
  Best Local Similarity   22.5%;  Pred. No. [illegible];
  Matches  131;  Conservative   68;  Mismatches  [illegible];  Indels  177;  Gaps  [illegible];

Qy      40 VQRGISVENS -  -WQIVR--RYSDF[illegible]N NS[illegible]A   --[illegible]PLLPKKL[illegible]N 83
Db     711 ISHNITFESSPPPVEWHISRTGQF[illegible]LM[illegible]HP[illegible]ARQ[illegible]LLESDLYKKV[illegible]PSFLV[illegible]S 770

Qy      84 M    DREFIADRQKGLQNYLNVI  [illegible]NHI[illegible]  SN[illegible]              ELVKK 117
Db     771 VWIKEDKE[illegible]      NSFNLLEMI[illegible]INLILWF[illegible]K[illegible]IVIA[illegible]NF[illegible]FVAVL[illegible]RIVEILQV 824

Qy     118 FLDPNNYSANYTHI  ALQQV[illegible]PEKWLVVI[illegible]W[illegible]EKKY [illegible]MEIENQPKEK 175
Db     825 F[illegible]LNNFN GVLEIVSAVNSV[illegible]V [illegible]LAQ            EKKEK 862

Qy     176 [illegible] 230
Db     863 [illegible]AVE[illegible]EKKYIVK [illegible] [illegible]

Qy     231 KC[illegible]YKAKPKDPPLKKY[illegible]NPKKI[illegible]IKIY[illegible]   R[illegible]ILFVIK  [illegible] 278
Db     914 K[illegible]EKK [illegible]KVA[illegible] 962

Qy     279 LHDKGFFYGHLHASNVML[illegible]N[illegible] 336
Db     963 LSEKK[illegible]LYLFNK[illegible]PENK [illegible]NA[illegible]HGS 1012

Qy     337 [illegible]HLLYEMIYGKFP[illegible]VPVD[illegible]FLA[illegible]A[illegible]VA  V[illegible]TA[illegible]KN  GMP[illegible]ISRLLQ 392
Db    1013 [illegible]   KGHL [illegible]LEEKEFYK[illegible] [illegible]VVGAP[illegible]NI[illegible]V[illegible]SD 1064

Qy     393 MF[illegible]SDVLL[illegible]KE[illegible]KI[illegible] [illegible]HQ[illegible]K[illegible]IKAQSHHG 451
Db    1065 HSVFLDVDLNSSCGSNTIFAPVLLPHSK[illegible]PSSS[illegible]          GSLEKL 1104

Qy     452 [illegible]EEKKK[illegible]LAKKK[illegible]AL[illegible]NN[illegible]NSS   PLISPSSLIPPS[illegible] 508
Db    1105 SEEPLIPPP[illegible]PPRKKFDHDAL  -   ---   NS[illegible]AVK[illegible]PPA[illegible]PPPKVK 1151

Qy     509    [illegible] 544
Db    1152 PRVPVLMGIFDGPVPSPPPPPPRDPLP[illegible]PPPVLLE[illegible]HH[illegible]N 1174


Search completed: June 12, 2002, 10:[illegible]7:4[illegible]
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```
OM protein - protein search, using sw model

Run on:          June 12, 2002, 09:53:49 ; Search time 94.83 Seconds
                                           (without alignments)
                                           584.663 Million cell updates/sec

Title:           US-09-684-458-2
Perfect score:   3001
Sequence:        1 MAEMEKPPAGKVLIIDVI..........PQKGIERKAKICDHSAPKIS 577

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters:      283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       PIR_71:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	195	6.5	1081	2	S51899	probable protein k
2	182	6.1	1851	2	T19964	hypothetical prote
3	171.5	5.7	1228	2	T18897	hypothetical prote
4	170.5	5.7	895	2	T15881	hypothetical prote
5	168.5	5.6	736	1	KIRBCE	protein kinase C (
6	167.5	5.6	737	1	S28942	protein kinase C (
7	166.5	5.5	737	1	KIMSCE	protein kinase C (
8	160	5.3	633	1	S49611	probable serine/th
9	158.5	5.3	1332	2	D83637	serine/threonine p
10	158	5.3	1206	2	T34021	protein kinase SK2
11	158	5.3	1241	2	T18932	serine/threonine pr
12	155.5	5.2	1233	2	T14157	serine/threonine p
13	154.5	5.1	967	2	E96636	hypothetical prote
14	153.5	5.1	737	1	KIRTCE	protein kinase C (
15	153.5	5.1	1621	2	T15264	hypothetical prote
16	153	5.1	576	2	T36729	probable serine/th
17	153	5.1	981	2	T34108	receptor kinase ho
18	152.5	5.1	1297	2	S25714	son of sevenless 2
19	150.5	5.0	1460	1	E3BEIF	immediate-early pr
20	149.5	5.0	1260	1	TVFTNU	protein-tyrosine k
21	149	5.0	676	1	S35704	protein kinase C (
22	149	5.0	1387	2	T16511	hypothetical prote
23	147.5	4.9	631	2	T09512	serine/threonine s
24	144	4.8	1255	1	A24571	protein-tyrosine k
25	143.5	4.8	612	2	T47743	receptor-like prot
26	143.5	4.8	1794	2	T38459	hypothetical diver
27	143	4.8	442	2	[illegible]	[illegible]
28	142	4.7	426	2	S71886	Ste20-like protein
29	142	4.7	820	2	T09645	hypothetical prote
30	142	4.7	1585	2	T31611	hypothetical prote
31	141	4.7	433	2	T46552	probable serine/th
32	141	4.7	1064	2	T13943	termin related pro
33	140	4.7	505	1	S77654	protein kinase pkn
34	140	4.7	982	2	T18476	serine threonine k
35	139	4.6	674	1	KIMSCD	protein kinase C (
36	138.5	4.6	613	2	T15499	hypothetical prote
37	138.5	4.6	981	1	FOMVAM	gag-abl polyprotei
38	138.5	4.6	1375	2	S48985	hypothetical prote
39	137.5	4.6	842	2	S60612	protein kinase CLA
40	137.5	4.6	1271	2	S37958	myosin heavy chain
41	137	4.6	304	2	H86342	12082.26 protein
42	137	4.6	673	1	KIRBCT	protein kinase C (
43	137	4.6	939	2	S28034	probable serine/th
44	137	4.6	1254	2	T48161	pi197 precursor
45	137	4.6	1737	2	A59565	unconventional myo

ALIGNMENTS

```
RESULT 1
S51899
probable protein kinase HRC1081 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein O0784; protein YOL100w
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 18-Aug-1995 #text_change 24-Sep-1999
C;Accession: S51899; S59175; S66796
R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
submitted to the EMBL Data Library, January 1995
A;Description: Sequence analysis of a 14kb DNA fragment of yeast chromosome XV includ
 and a Delta.
A;Reference number: S51848
A;Accession: S51899
A;Molecule type: DNA
A;Residues: 1-1081 <VAN>
A;Cross-references: EMBL:Z48149; NID:g663234; PIDN:CAA88162.1; PID:g663254
R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
Yeast 11, 1069-1075, 1995
A;Title: Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including
a delta element.
A;Reference number: S59156; MUID:96077[illegible]
A;Accession: S59175
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1081 <VAW>
A;Cross-references: EMBL:Z48149; NID:g663234; PIDN:CAA88162.1; PID:g663254
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 199
R;Durand, P.; Hilger, F.; Portetelle, D.; Vandenbol, M.
submitted to the Protein Sequence Database, July 199
A;Reference number: S66791
A;Accession: S66796
A;Molecule type: DNA
A;Residues: 1-1081 <DUR>
A;Cross-references: EMBL:Z74842; NID:g1420[illegible]; PIDN:CAA99115.1; PID:e251892; PID:g14
A;Experimental source: strain S288C
C;Genetics:
A;Map position: 15L
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C;Keywords: ATP; phosphotransferase
F;177-443/Domain: protein kinase homology <KIN>
F;185-193/Region: protein kinase ATP-binding motif

  Query Match             6.5%;  Score 195;  DB 2;  Length 1081;
  Best Local Similarity   21.4%;  Pred. No. [illegible];
  Matches  [illegible];  Conservative   74;  Mismatches  [illegible];  Indels  144;  Gaps   [illegible];

Qy        161 KKYFLMKIENLPEERIVLSWAPL[illegible] 220
              [illegible]
Db        212 FKEYAAFVLN  FFYLIFL [illegible] SIFQDES 2[illegible]

Qy        221 [illegible]
```

```
Db    252 YYELLEYAENTEEEGLMKKYGGLDEIAARY                  ---YAAQIIDAIDYLH 295

Qy    290 LKEFFYGHLHASNVMLDGD            IPRLLDLENSLIGLPSFYRSYFSQFRKINILE 331

Db    296 LNIIHRDIKPENILLGEMKIKLIDFGIAKLLNPINNSVSKPEYDLSIRSK SFVGIAE 354

Qy    332 DV                  DVHCFGHLLYEMIYGRPPDSVPVD                SFPPAPSM 365

Db    355 YVSPELLNDSFIIYPSDIWAPGIILFQMIAGKPPFKAINEYLTFQKVMKVQYAFIPGFPL 414

Qy    366 AVVAVLESTLSCEACKN GMPTISRLLQMPLESDVLL  ------TISEKPQFKIPTKL 415

Db    415 IFPDLVKKIL     VKNLDPRKLIISQIKEHHFFKDLNFKPLSVWSKIPPSIKPYKINAKS 470

Qy    416 KEAL          RIAKECI     EKRLIEEQK       QIHQHRRLTRAQSHHGSEEERKKR 459

Db    471 MQAMGGGGDFKIVKKSVNIDIKSHLVIQKGASSPSVEEIIHSILYNNNIHASIESEISIK 530

Qy    460 KIIARKKSKRSA  LEN                                 SEFHSARYSNSN 486

Db    531 K    RPIDERIAQILENAEKINNEENQIGEEIEKIAAAAALAAAAALIEKIMQSYPTLS 587

Qy    487 NGGSGASSPLIS                PSSPTPP SISGISALPPPPPPPLPPAAPLPPA 530

Db    588 GKGGEGGGEAIIGRPITYKKLGGIEGKPIAKSPPLSASVISSKVPMPPYIPPMSPPMIPY 647

Qy    531 GEISA

Db    648 GDGIG
```

RESULT 2
I1?064
hypothetical protein C46G2.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: I1?064
R;McMurray, A.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z1?204
A;Accession: I1?064
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1851 <WIL>
A;Cross-references: EMBL:Z68296; PIDN:CAA92591.1; GSPDB:GN00?22; CESP:C46G2.1
A;Experimental source: clone C46G2
C;Genetics:
A;Gene: CESP:C46G2.1
A;Map position: 4
A;Introns: [illegible]

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  Query Match             6.1%;  Score 182;  DB 2;  Length 1851;
  Best Local Similarity   22.2%;  Pred. No. 0.028;
  Matches  105;  Conservative   61;  Mismatches  160;  Indels  146;  Gaps   22;

Qy    176 IVLSWADLGPDKY  LSDKDFQCLIKLLPSCLHPYIYRVIFATANESSAI  ------LI 225

Db    368 VAVAWCELQESKLNKIERQRFREEAEMLKDLQHPNIVR  FYDYWESADLCKRKYIVLV 425

Qy    226 RMFNEKCILEELIYEAKRKPPPLKKY  CNPKKIQGLEDQQIKIYGRQILEVLKFLHDKG 283

Db    426 TELMISGTLK              MYLKRFKKRINIEVV        LKSWCRQILKGLSFLHTRN 468

Qy    284 PPYGH  LHASNVMLDGD          PRLLDLEN      SLIGLPSF       YRSYFSQF 324

Db    469 PPVIHRDLKCDNIFIICLDGSVKIGDLGLATLKNKSFAKSVIGTPEFMAPEMYEEMYD   526

Qy    325 RKINILESVDVHCFGHLLYEMIYGRPPDS                   -  VPVDSFP  PAPSMAV 367

Db    527          ESVDVYAFGMCLLEMVTGEYPYGECMNPAQIYRKVISGVKPESFSKIPAQYPEI 580

Qy    368 VAVLESTLSCEACKNGMPTISRLLQMPLESD                          VLL 401

Db    581 KEIIDRCIRVK  REERSTVKQLLVDDFFIPEDLIGIRVEIKNRDADLNDLNVEIQMQLR 638

Qy    402 TISEKPQFKIPIKLKEALRIAKEC          IEKRLIEEQ                   434

Db    639 VYDEKKKKQYRFKENEGIQFAFDIENDSPDKVVQQMIEQQHIPDEDTRMITKLIKDKVDA 698

Qy    435  KQIHQHRRLTRAQSHHGSEEERKKRKKIIARKKSKRSALENSEFHSARYSNSNNSGSGAS 493

Db    699 FRRDRDHRLL---EIKRAKEEEERIREEAEIEKRIRKAEAKREKKERLEKERLEEAAA 755

Qy    494 SPLTSPSSPTPPSTSGISALPPPPPPPPPPA -APL-PPASIEVPAQLSSQA 542

Db    756 AAAANP NPTP             IPPIPATPHSSAQQQPIPPPLSIQISAEIQQSA 798
```

RESULT 3
T18897
hypothetical protein C04A11.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 17-Oct-1999 #sequence_revision 17-Oct-1999 #text_change 18-Feb-2000
C;Accession: T18897
R;McMurray, A.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19041
A;Accession: T18897
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1228 <WIL>
A;Cross-references: EMBL:Z81460; PIDN:CAB03829.1; GSPDB:GN00028; CESP:C04A11.3
A;Experimental source: clone C04A11
C;Genetics:
A;Gene: CESP:C04A11.3
A;Map position: X
A;Introns: [illegible] 1117/3; 11

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  Query Match             5.7%;  Score 171.5;  DB 2;  Length 1228;
  Best Local Similarity   22.2%;  Pred. No. 0.063;
  Matches  113;  Conservative   63;  Mismatches  188;  Indels  145;  Gaps   22;

Qy    111 NNDSANY[illegible]   FIPKKIEL  NRLR 169

Db      9 NLERANQAEKKLPSY  IYDNVNPKDHWNI[illegible]KAVSKI[illegible]AASKSIE 67

Qy    170 NQPKFRIVISWADLGPDKYISDKDFQCLIKLLPSCL HPYIYRVIFATANESSALLIRMF 228

Db     68 IQEGEEL                   EDFLVEIEIILSDCKGHPVMLGLYSTYPFENKLIMLLEF 112

Qy    229 [illegible]GPPYGH 288

Db    113 CGGGAVDNIIVELG                      HVLKEDQIRYIGYYVCDALKWLHSQNVIHRD 157

Qy    289 LHASNVMLDGD ICRLLDL                ENSLIGLPSFYRSYFSQFRKINILESV - 333

Db    158 LKACNILLIQDGQVRLADFGVSAKLKSERKKRDTFIGTP    -- YWMAPEVMACEIPKD 211

Qy    334 -------DVHCFGHLLYEMIYGRPPDSVPVDSFPPAPSMAVVAVLESTLSCEACKNGMPT 386

Db    212 QPYDCISDIWSFGITLIEMAQGEPPHS----------DVSVMRVI-----IKVQKSEPPT 256

Qy    387 ISRLLQ----MPLFSDVLLTISEK-PQFKIPTKLKEALRIAKECIEKRLIEEQKQIHQHR 441

Db    257 --LLQPSHWIRSPSDILIRCLVKDPRNRPPA-  -                  --  AEIFKHQ 292

Qy    442 KLIKAQSHHGSEEERKKRKKIIARKKSK              KSALENSEFHSARYSNSNN 487

Db    293 WFQNAPS-      - KKKMIMDLLAEMYADVQEEVVIDGDEESVAGSDEISQKRGDSWS 343

Qy    488 SGSGASSPLTSPSSPTPPSTSGISALPPPPPPPPPPAAPLPPASTEVPAQLSSQAVNGMS 547

Db    344 SASDSPRPATSDGFKVPIVSVPIIETPPPLTPHKKRAAPPPP  QEVNAHRQSPVVNG    399
```

```
Qy    519 KGALLSSL--NLKGTLRKAKTDHSAP 374
Db      4 KEAENSSFAEESFSNSNISSEGIAEFSIP 428
```

RESULT 4
T15881
hypothetical protein D1044.- - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: [illegible] Sep 1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15881
R;Fraley, A.
submitted to the EMBL Data Library, [illegible] 1994
A;Description: The sequence of C. elegans cosmid D1044.
A;Reference number: Z18423
A;Accession: T15881
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1895 <PAR>
A;Cross-references: EMBL:[illegible]; NID:g495681; PID:g495684; PIDN:AAA50735.1; CESP:D1044.3
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:D1044.3
A;Introns: [illegible]

Query Match [illegible]; Score 170.5; DB 2; Length 1895;
Best Local Similarity [illegible]; Pred. No. 0.12;
Matches [illegible]; Conservative [illegible]; Mismatches 203; Indels 229; Gaps 48;

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Qy    [illegible] IEVQRKL [illegible] SVENE [illegible] FLP 2[illegible]
Db    [illegible] 285
Qy    [illegible] EKK [illegible] HVITINE 1[illegible]
Db    [illegible] EKAV [illegible] KENVIIDET 341
Qy    [illegible] ELVKKFLDPNNYLA NYIEIALQQ 1[illegible]
Db    342 [illegible]
Qy    [illegible]
Db    [illegible]
Qy    [illegible]
Db    [illegible]
Qy    224 [illegible]
Db    515 [illegible]
Qy    [illegible]
Db    [illegible]
Qy    331 [illegible]
Db    [illegible] VEHST-------NMLLLAM [illegible]
Qy    [illegible]
Db    [illegible] GVKLLEYLEDVAK 708
Qy    [illegible] SFKSALENSFEESAFYSNSNNSGSGASSP 495
Db    [illegible]
Qy    [illegible] SPSS [illegible] --PPPPEPPPAAPEPPASTEVPAQL 538
```

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Db    759 INPAPRRNHSMSAGETPRSSIV [illegible] 818
Qy    539 SSQA---VNGMSRGALLSS 554
Db    819 SSSTELKVSKQSDGLTVSS 837
```

RESULT 5
KIRBCE
protein kinase C (EC 2.7.1.-) epsilon - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1992 #sequence_revision [illegible] Sep 1992 #text_change 21-Nov-1997
C;Accession: A29880
R;Ohno, S.; Akita, Y.; Konno, Y.; [illegible], K.
Cell 53, 731-741, 1988
A;Title: A novel phorbol ester receptor/protein kinase, nPKC, distantly related [illegible]
A;Reference number: A29880; MUID:8822[illegible]367
A;Accession: A29880
A;Molecule type: mRNA
A;Residues: 1-736 <OHN>
A;Cross-references: GB:M20014
C;Function:
A;Description: catalyzes the formation of peptidyl serine phosphate or peptidyl threo[illegible]
A;Note: activity is calcium independent, phospholipid dependent, and activated by dia[illegible]
C;Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology; [illegible]
C;Keywords: ATP; autophosphorylation; duplication; phorbol ester binding; phosph[illegible]
F;156-161/Region: pseudophosphorylation motif
F;170-220/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F;243-292/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F;405-667/Domain: protein kinase homology <KIN>
F;413-421/Region: protein kinase ATP-binding motif
F;170,201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;243,274,276,292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;436,455,531,533/Active site: Lys, Glu, Asp, Lys #status predicted
F;702,709/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status p[illegible]

Query Match 5.6%; Score 1[illegible]; DB 1; Length 736;
Best Local Similarity 23.2%; Pred. No. [illegible];
Matches [illegible]; Conservative 48; Mismatches [illegible]; Indels [illegible]; Gaps 1[illegible];

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Qy    [illegible] 217
Db    [illegible] 479
Qy    [illegible] 2[illegible]
Db    477 [illegible] 520
Qy    [illegible] 324
Db    [illegible] 5[illegible]
Qy    427 [illegible] 372
Db    [illegible] 638
Qy    [illegible] 417
Db    [illegible] 695
Qy    418 [illegible] 434
Db    696 NFDQDFTREEPVLTLVDEAIVKQINQFF 72[illegible]
```
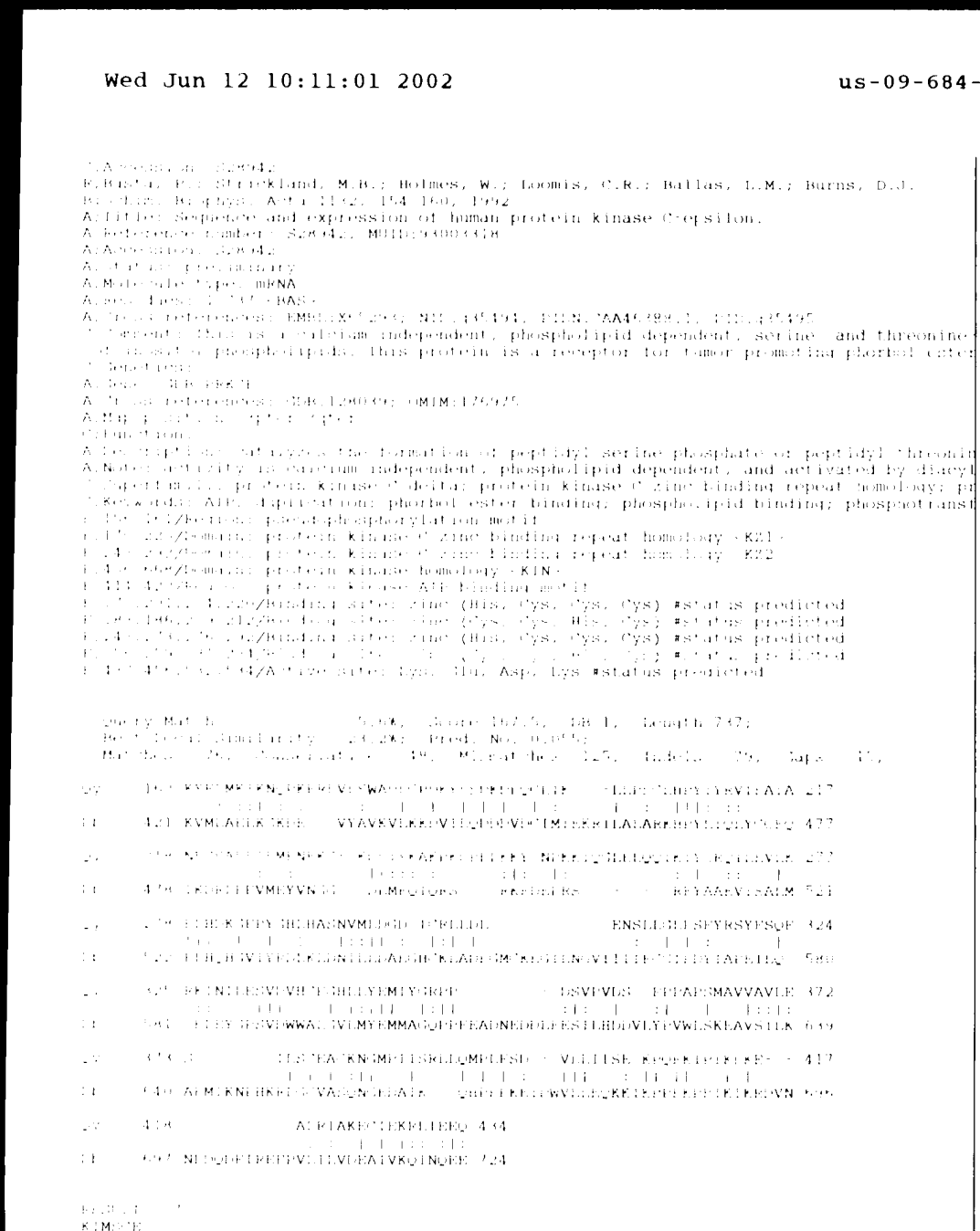
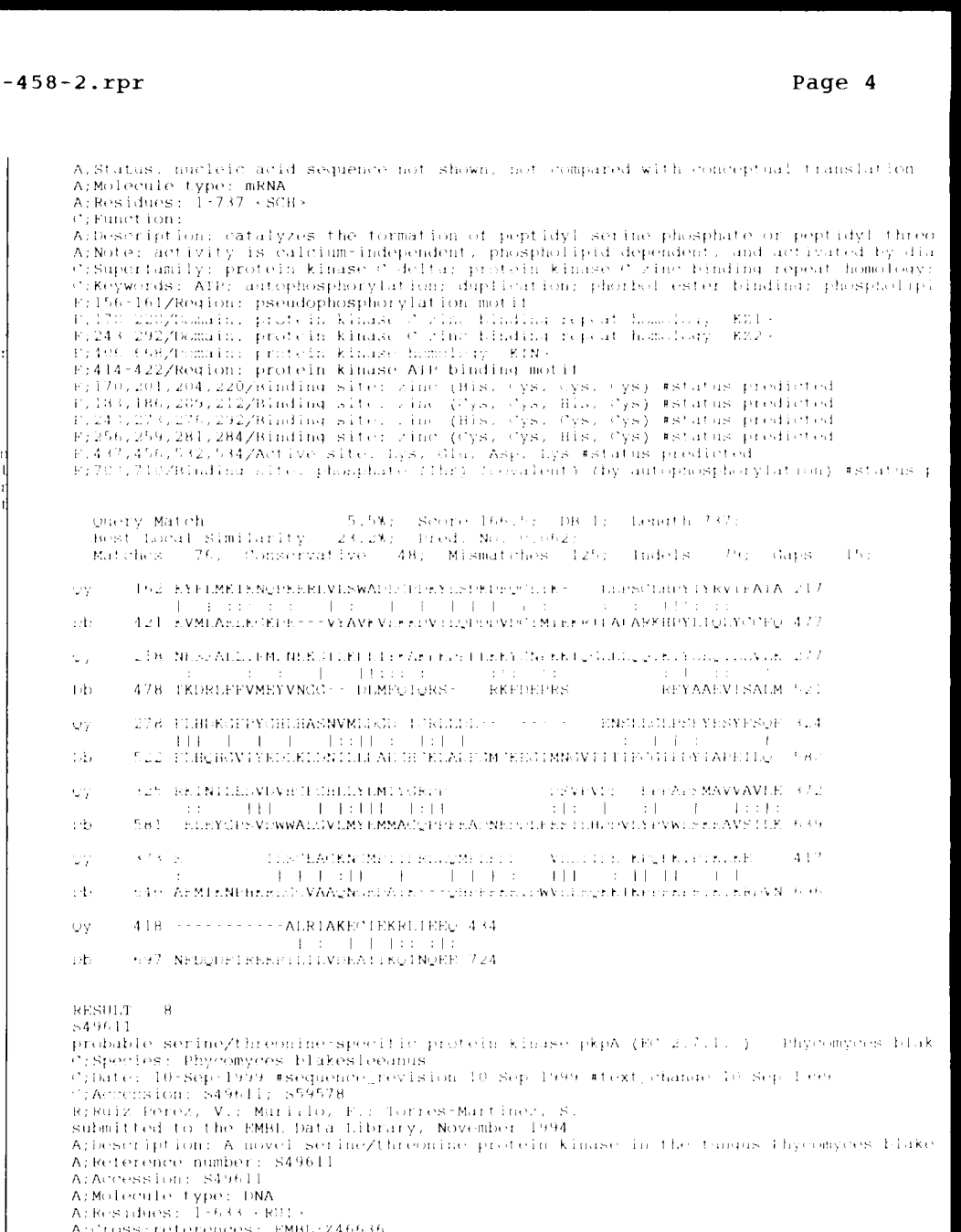
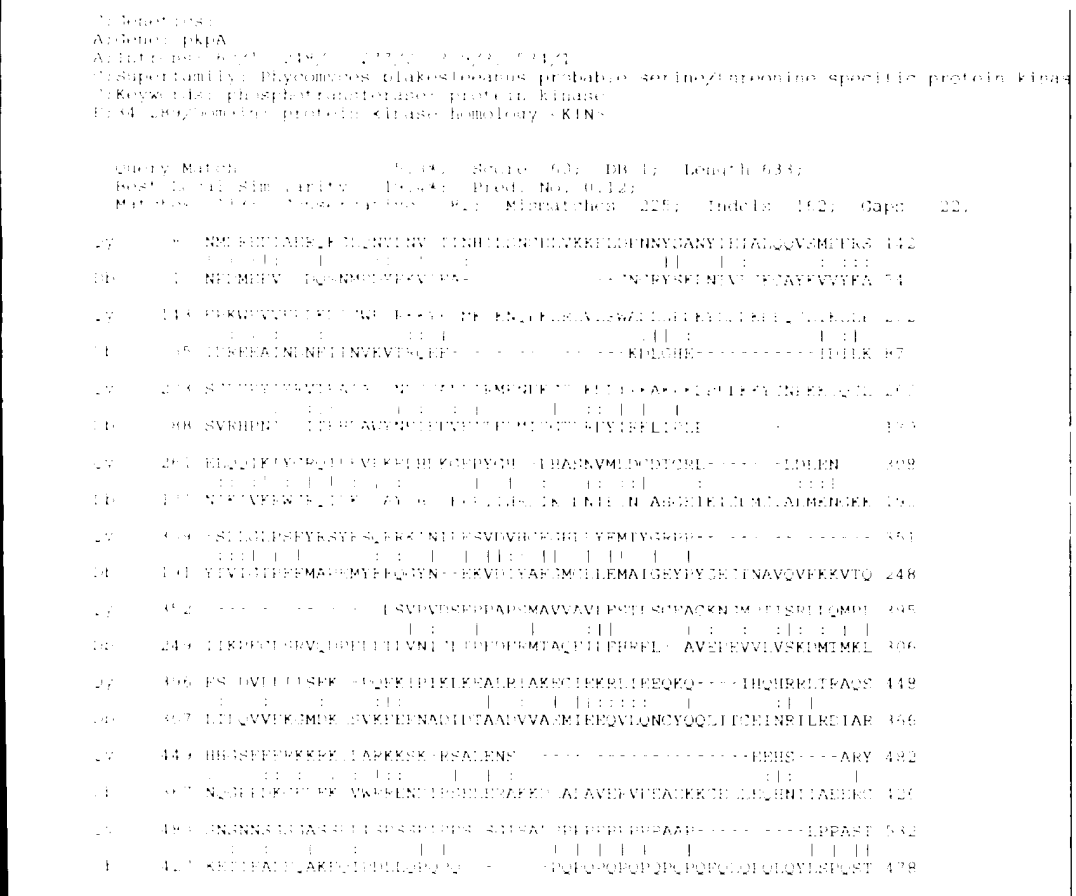
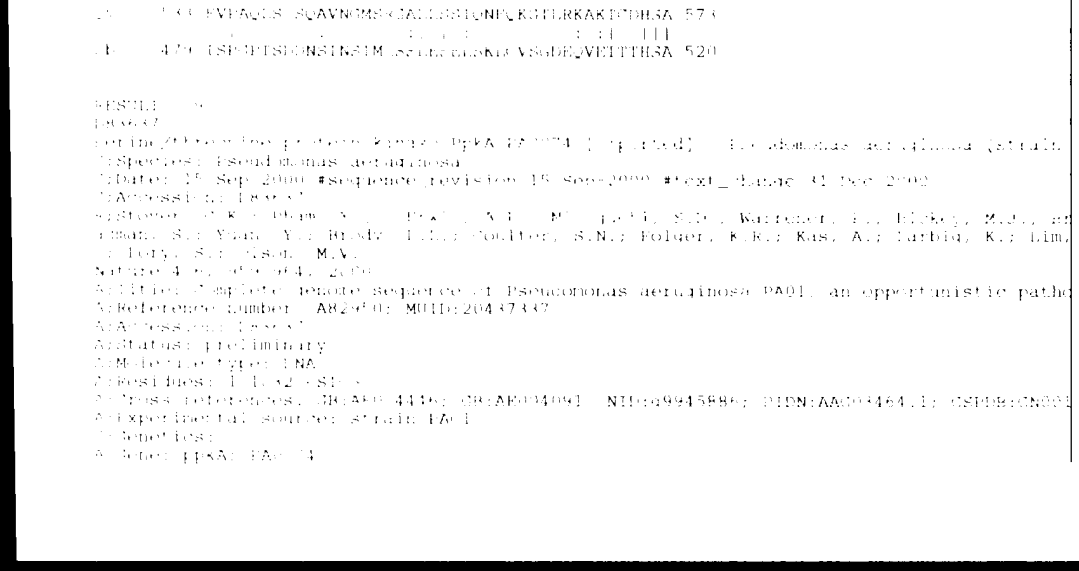
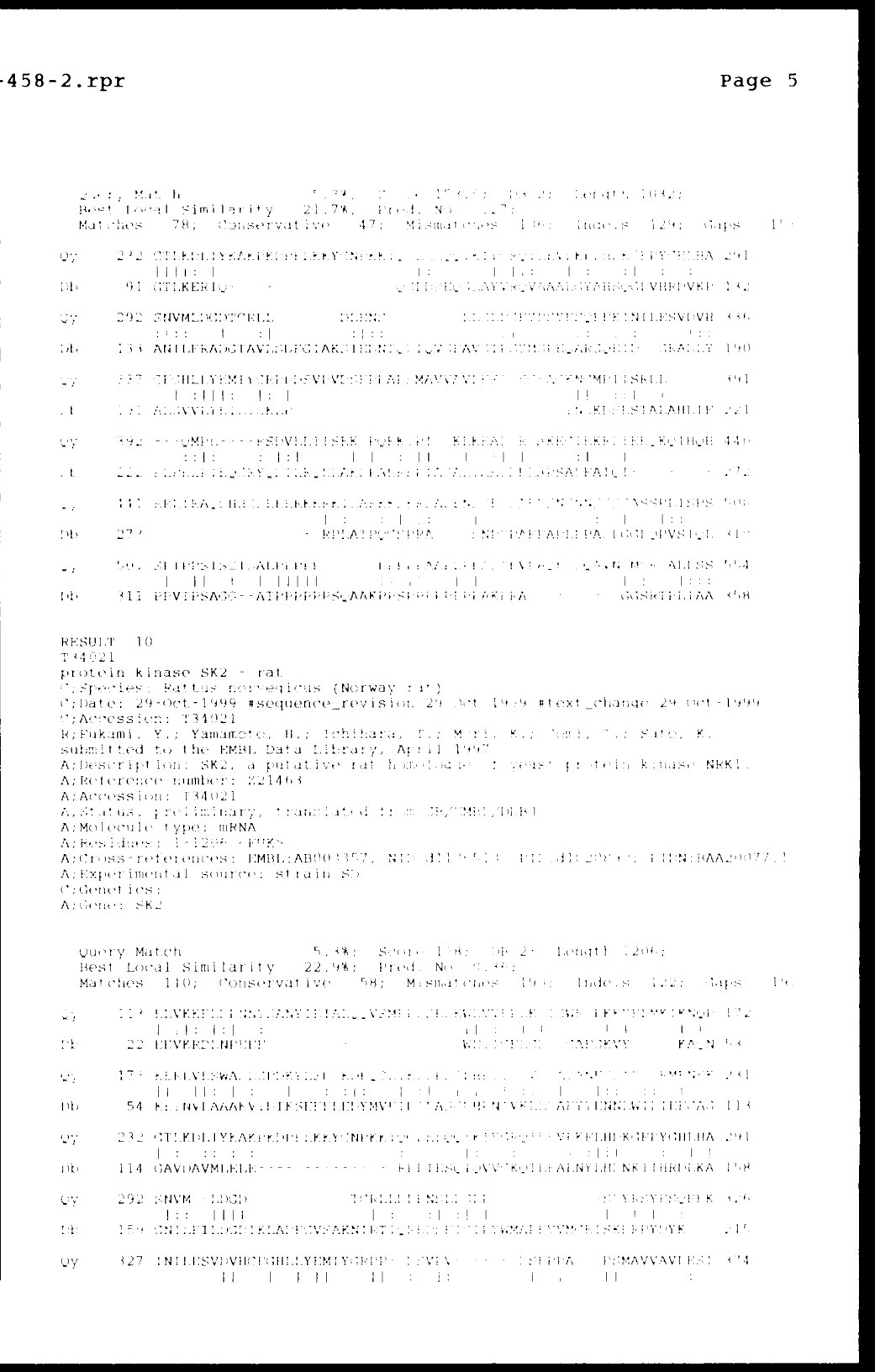

RESULT 6
S28942
protein kinase C (EC 2.7.1.-) epsilon - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jun-1999

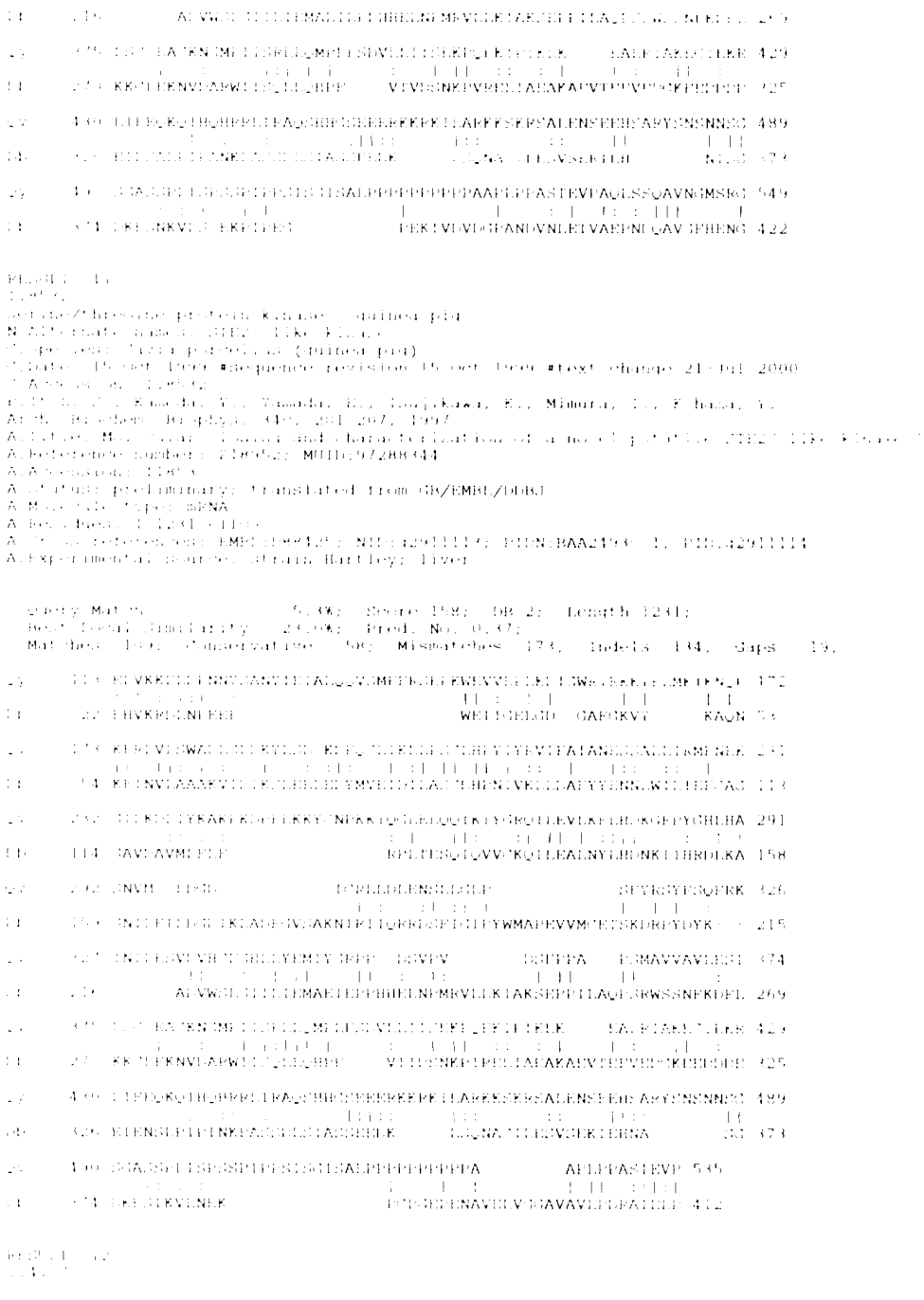












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  Query Match             5.1%;  Score 154.5;  DB 2;  Length 907;
  Best Local Similarity   19.5%;  Pred. No. 0.39;
  Matches  1[illegible]2;  Conservative  6[illegible];  Mismatches  1[illegible]1;  Indels  20[illegible];  Gaps  22;

Qy     [illegible] [illegible]INN[illegible]GNM[illegible]IALAQKGLQNT[illegible]NV[illegible]NH[illegible]LSNCHLVK [illegible]
Db     11[illegible] DLSI[illegible]DGSP[illegible]VRK[illegible]DV[illegible]M - - - VMH[illegible]MKD[illegible]QK[illegible]CPP[illegible]HSHIMP [illegible]IP 159

Qy     117 K[illegible]NNY[illegible]ANV[illegible]IA[illegible]LV[illegible]MFF[illegible]KWEVVEI[illegible]K[illegible]     W[illegible]KKYE[illegible]MKI 168
Db     1[illegible] R---------ANV[illegible]KV     [illegible]HEFNA     [illegible]IK[illegible]WIT[illegible]NEIWI[illegible]KSKYW[illegible]SV 1[illegible]9

Qy     1[illegible]9 KN[illegible]KE[illegible]VL[illegible]WA[illegible] [illegible]KDP[illegible]IK[illegible]HPYIYRVTFAIANPSALLIPMF 228
Db     1[illegible] GKNQ[illegible]V--------KKVIAAI[illegible]-------------------------LIKMS 221

Qy     229 NFK[illegible]K[illegible]IYK[illegible]NEKK[illegible]IK[illegible]VIK[illegible] 2[illegible]
Db     222 KFKFDMMEIDKKKKKK -----------KS[illegible] 2[illegible]

Qy     2[illegible] [illegible]SKIIIINK[illegible]     SFTRS[illegible]YF[illegible]EKKINIIESVIVH[illegible] 3[illegible]
Db     2[illegible]8 SKNS[illegible]SP[illegible]ESVL[illegible]MM[illegible]FCRV[illegible]DFANSASHLIWNMRVQALEKLSPIDVKRLA 325

Qy     3[illegible] [illegible]IYEMIYGRFF[illegible]SVIVDSFFFA[illegible]SMAVVAV[illegible]CEACKNGMP[illegible]IKRLLQMP[illegible] 3[illegible]8
Db     32[illegible] IHI[illegible]SQKEAQEPNESNIED------VISVVE---------[illegible] 351

Qy     3[illegible] V[illegible]IAKE[illegible]IEKK[illegible]EELT[illegible]A[illegible]HHGSIEEHKK 4[illegible]9
Db     3[illegible]2 IKQKKIEIESII[illegible]VKMEHEESVNLDEESVV   [illegible]NCEQDTI                  388

Qy     45[illegible] [illegible]KE[illegible]A[illegible]N[illegible]     [illegible]IAK[illegible]N[illegible]N          N[illegible]CA[illegible]LI[illegible]F 49[illegible]
Db     [illegible]          MK[illegible]NP[illegible]KYFN[illegible]IKIAPILFSI 41[illegible]

Qy     5[illegible] SSPTPPSISIISAIPP[illegible]PPPIPFAA  -  --------PLPPA 530
Db     44[illegible] [illegible]PIA[illegible]IAISM[illegible]PPPPP[illegible]PFFAVMFLKHFAPPPPPPLPPA 48[illegible]
```

RESULT 14
KIBPCE
protein kinase C (EC 2.7.1.[illegible]) epsilon - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 11-Jun-1999
C;Accession: B28[illegible]; B2[illegible]40[illegible]; S0[illegible]216
R;Ono, Y.; Fujii, T.; [illegible], K.; Kikkawa, U.; Igarashi, K.; Nishizuka, Y.
J. Biol. Chem. 263, 6927-6932, 1988
A;Title: The structure, expression, and properties of additional members of the protein
A;Reference number: A92[illegible]; MUID:88198270
A;Accession: B28[illegible]
A;Molecule type: DNA
A;Residues: 1-737 <ONO>
A;Cross-references: GB:M18331; NID:g206182; PIDN:AAA41872.1; PID:g206183
R;Housey, G.M.; O'Brian, C.A.; Johnson, M.D.; Kirschmeier, P.; Weinstein, I.B.
Proc. Natl. Acad. Sci. U.S.A. 84, 1065-1069, 1987
A;Title: Isolation of cDNA clones encoding protein kinase C: evidence for a protein kina
A;Reference number: A94145; MUID:87147193
A;Accession: B2[illegible]4[illegible]
A;Molecule type: mRNA
A;Residues: [illegible]-4[illegible],'[illegible]HDDREE[illegible]PGSGAE[illegible]',467,'LSNPFLLLLPDQ[illegible]PPLLRQ',487-545,'C',547-636
A;Cross-references: GB:M15[illegible]; NID:g20[illegible]92; PIDN:AAA41877.1; PID:g206193
C;Comment: protein kinase C eps[illegible]lon and epsilon' appear to be encoded by the same gene [illegible]
C;Function:
A;Description: catalyzes [illegible] peptidyl serine phosphate or peptidyl threon[illegible]
A;Note: activity is calcium-independent, phospholipid-dependent, and activated by diacyl
C;Superfamily: protein kinase C delta; protein kinase C zinc-binding repeat homology; pr
C;Keywords: alternative splicing; ATP; autophosphorylation; duplication; phorbol ester b
F;15[illegible]-1[illegible]2/Region: pseudophosphorylation motif
F;170-220/Domain: protein kinase C zinc-binding repeat homology <KZ1>
F;243-292/Domain: protein kinase C zinc-binding repeat homology <KZ2>
F;406-668/Domain: protein kinase homology <KIN>
F;414-422/Region: protein kinase ATP-binding motif
F;17[illegible],201,204,220/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;183,186,209,212/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;2[illegible],2[illegible],2[illegible],292/Binding site: zinc (His, Cys, Cys, Cys) #status predicted
F;256,259,281,284/Binding site: zinc (Cys, Cys, His, Cys) #status predicted
F;437,4[illegible],[illegible]2,5[illegible]4/Active site: Lys, [illegible], Asp, Lys #status predicted
F;703,710/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status p

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  Query Match             5.1%;  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   22.9%;  Pred. No. 0.34;
  Matches  75;  Conservative  47;  Mismatches  12[illegible];  Indels  79;  Gaps  1[illegible];

Qy     162 KYFLMKIKNQPKEKLVLSWADLGPQKYLSDKLFQ[illegible]IK     LLPSCLPLYIYRVTFAIA 217
Db     4[illegible] [illegible]VMLAL[illegible]     VVAVEV[illegible]     [illegible]LIQLYC[illegible]FQ 477

Qy     21[illegible] N[illegible]SAL[illegible]IEMFNLE[illegible]IKELLIY[illegible] 277
Db     478 TKERLFFVMEYVNGG[illegible]  LLMFQIQKS     FKE[illegible]          [illegible]YAAEVT[illegible]ALM 521

Qy     278 FLHDKGFPYCHLHASNVMLDSD[illegible]TGKLI[illegible]          [illegible]NSLLGLFSPYKSYFSQF 324
Db     522 FLHQRGVIYRDLKLDN[illegible]LLDAE[illegible]KLA[illegible]M[illegible] [illegible]NGV[illegible]IAPEI[illegible] 580

Qy     325 KKINFLESVDVHCFGHLLYEMIYGFPP[illegible]  -  D[illegible]VIV[illegible] [illegible]FFFAFSMAVVAVLE 372
Db     581 ELEYGPSVDWWALGVLMYEMMAGQPP[illegible]EAENE[illegible]LFE[illegible]IL[illegible]VLYPVWLSKEAVSI[illegible]K 639

Qy     373 S          TLSCEACKNGMPTISPLLQMPLPGD   VILLISF[illegible]KP[illegible]PKIPIELKE    41[illegible]
Db     640 A[illegible]IE[illegible]NG[illegible]VAA[illegible]NG[illegible]    [illegible]KRPVN 696

Qy     418           [illegible]IAKE[illegible]IEKRLIEEQ 434
Db     697 NFDQDFTREEPILTLVDEAIVKQINQEE 724
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RESULT 15
T15264
hypothetical protein F59E12.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15264
R;Johnson, D.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid F59E[illegible].
A;Reference number: Z18318
A;Accession: T15264
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1621 <JOH>
A;Cross-references: EMBL:AF003386; NID:[illegible]; PID:[illegible]; PIDN:AAB542[illegible].1; GSPDB
A;Experimental source: strain Bristol N2; clone F59E12
C;Genetics:
A;Gene: CESP:F59E12.9
A;Map position: 2
A;[illegible]

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  Query Match             5.1%;  Score 1[illegible];  DB 2;  Length 16[illegible];
  Best Local Similarity   19.5%;  Pred. No. 0.44;
  Matches  114;  Conservative  79;  Mismatches  [illegible]91;  Indels  [illegible]1;  Gaps  29;

Qy     1[illegible] NV[illegible]NHIL[illegible]N[illegible]LVEKFLI[illegible]N     [illegible]FKGPVV[illegible]FDI 155
Db     868 NIGTT     ENCPMLIVVLRPNFAERP[illegible]     [illegible]FKLMQI 91[illegible]

Qy     156 GWKIRKKYFLMKIKNQPKEKLVLSW     AD[illegible]     [illegible]KYLS[illegible]KLLSCLHP 20[illegible]
Db     917 SWKQ[illegible]     ENEEKE     [illegible]NISEAVNESIES -     962
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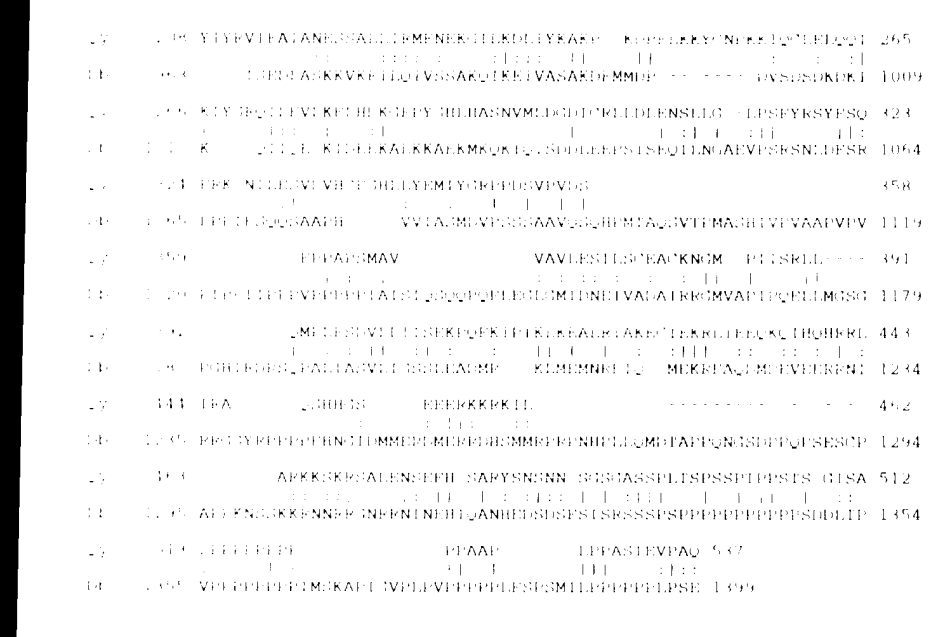

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 12, 2002, 09:53:44 ; Search time 106.75 Seconds
(without alignments)
600.371 Million cell updates/sec

Title: US-09-684-458-2
Perfect score: 8001
Sequence: 1 MAPMEK[illegible] ....[illegible] 577

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, [illegible] residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: [illegible]
Maximum DB seq length: [illegible]

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*
1: [illegible]AA1980.DAT:*
2: [illegible]
3: [illegible]
4: [illegible]
5: [illegible]AA1984.DAT:*
6: [illegible]AA1985.DAT:*
7: [illegible]
8: [illegible]
9: [illegible]AA1988.DAT:*
10: [illegible]AA1989.DAT:*
11: [illegible]AA1990.DAT:*
12: [illegible]
13: [illegible]
14: [illegible]
15: [illegible]
16: [illegible]
17: [illegible]
18: [illegible]
19: [illegible]
20: [illegible]
21: [illegible]
22: [illegible]

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	[illegible]	10[illegible]	577	22	AAF02775	Human PRO C MG.2 p
2	[illegible]	[illegible]	[illegible]49	22	AAB65680	Novel protein kina
3	874	2[illegible].1	[illegible]63	22	ABB594[illegible]5	Drosophila melanog
4	8[illegible]	2[illegible].5	155	21	AAB32[illegible]78	Human secreted pro
5	575	1[illegible].2	141	22	AAU17470	Novel signal trans
6	[illegible]2.5	1[illegible].1	515	22	ABB62[illegible]63	Drosophila melanog
7	[illegible]2.5	1[illegible].1	515	22	ABB62[illegible]72	Drosophila melanog
8	[illegible]32	1[illegible].1	157	21	AAB32[illegible]77	Human secreted pro
9	2[illegible].5	[illegible].1	496	22	AAM38834	Human polypeptide
10	[illegible]1.5	[illegible].0	495	22	AAM40620	Human polypeptide
11	[illegible]	[illegible].8	[illegible]	20	AAW87[illegible]2	Human serum glucoc
12	199.5	6.6	912	20	AAY[illegible]	Human GEK2 protein
13	199.5	6.6	968	20	AAY[illegible]	Full length human
14	195	6.5	1081	21	AAY[illegible]	Amino acid sequenc
15	180.5	6.0	911	20	AAY[illegible]57	Mouse STE20-relate
16	172.5	5.7	446	22	AAB[illegible]	Novel protein kina
17	172.5	5.7	1533	22	AB[illegible]	Novel human diagno
18	172	5.7	1513	22	AA[illegible]531	Human protein kina
19	171.5	5.7	502	22	AAM[illegible]	Human polypeptide
20	164.5	5.5	1043	22	ABB[illegible]	Drosophila melanog
21	162.5	5.4	407	22	ABB[illegible]	Drosophila melanog
22	162	5.4	873	22	AAM[illegible]	Human protein SEQ
23	161	5.4	541	19	AAW[illegible]7148	Mammalian Ena (Men
24	160.5	5.3	754	22	AAB[illegible]	Human protein sequ
25	158.5	5.3	591	22	AAM[illegible]	Human polypeptide
26	157.5	5.2	661	22	AAE[illegible]	Human protein kina
27	157.5	5.2	661	22	AAE[illegible]	Human protein kina
28	157.5	5.2	1189	22	ABB[illegible]9904	Drosophila melanog
29	157.5	5.2	1920	22	AAB[illegible]	Novel protein kina
30	156	5.2	429	21	AAY[illegible]	Human serum and gl
31	155.5	5.2	227	22	AAM[illegible]	Human polypeptide
32	155.5	5.2	464	22	AAM[illegible]	Human polypeptide,
33	155.5	5.2	1069	22	AAB[illegible]	Human protein kina
34	155.5	5.2	1202	21	AAB[illegible]	A murine Ste20-rel
35	15[illegible].5	5.1	894	22	AAM[illegible]	Human protein SEQ
36	15[illegible].5	5.1	1297	16	AAR[illegible]	mSOS2 protein. Mu
37	153	5.1	1504	22	AAB[illegible]	Human protein sequ
38	152.5	5.1	1068	22	AAM7[illegible]	Human protein SEQ
39	152.5	5.1	1078	22	AAM[illegible]	Human polypeptide
40	152.5	5.1	1089	22	ABG[illegible]	Novel human diagno
41	152.5	5.1	1297	14	AAR4[illegible]	Mammalian son of s
42	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	Human serine threo
43	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	Human polypeptide
44	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	Novel signal trans
45	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	Human KHS[illegible] protein

ALIGNMENTS

RESULT 1
AAF02775
ID AAF02775 standard; Protein; 577 AA.
XX
AC AAF02775;
XX
DT 06 AUG 2001 (first entry)
XX
DE Human PRO C MG.2 protein [illegible] cDNA clone.
XX
KW [illegible] gene therapy; [illegible] hypertrophy;
KW congestive heart failure; CHF; myocardial infarction; aortic stenosis;
KW [illegible] vaccine;
KW endothelial disease; DNA-C-MG.2 [illegible] cDNA; PRO-C-MG.2 protein.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 16..122
FT /label= PX_kinase_domain
FT Modified-site 32..36
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 54..58
FT /note= "cAMP and cGMP dependent protein kinase
FT phosphorylation site"
FT Modified-site 57..61
FT /note= "Casein kinase II phosphorylation site"
FT Modified site 110..114
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 116..125
FT /note= "Tyrosine kinase phosphorylation site"
FT Modified site 179..183
FT /note= "Casein kinase II phosphorylation site"
FT Modified-site 190..194

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FT                   /note= "Casein kinase II phosphorylation site"
FT   Modified-site   219..222
FT                   /note= "Casein kinase II phosphorylation site"
FT   Domain          25..264
FT                   /label= Pkinase domain
FT   Modified-site   255..257
FT                   /note= "Casein kinase II phosphorylation site"
FT   Region          290..311
FT                   /note= "Leucine zipper pattern"
FT   Modified-site   [illegible]
FT                   /note= "Casein kinase II phosphorylation site"
FT   Modified-site   441..445
FT                   /note= "cAMP- and cGMP-dependent protein kinase
FT                   phosphorylation site"
FT   Modified-site   452..456
FT                   /note= "Casein kinase II phosphorylation site"
FT   Modified-site   464..468
FT                   /note= "cAMP- and cGMP-dependent protein kinase
FT                   phosphorylation site"
FT   Modified-site   470..474
FT                   /note= "Casein kinase II phosphorylation site"
FT   Modified-site   480..495
FT                   /note= "N-myristoylation site"
FT   Modified-site   [illegible]
FT                   /note= "N-myristoylation site"
FT   Modified-site   [illegible]
FT                   /note= "N-myristoylation site"
XX
PN   W0200[illegible] A2.
XX
PD   [illegible] APR 2001.
XX
PF   [illegible] OCT 2000; 2000WO-US27512.
XX
PR   07-OCT-1999;   99US-0158587.
PR   [illegible]-OCT-1999;   99US-0162611.
XX
PA   (GETH ) GENENTECH INC.
PA   (CURA ) CURAGEN CORP.
XX
PI   Gerritsen ME,  Goddard A,  Grimaldi JC,  Mehraban F;
XX
DR   WPI; 2001-[illegible].
DR   N-PSDB; AA[illegible].
XX
PT   Polypeptides critical for angiogenesis and vascularization, and the
PT   nucleic acids encoding them, useful for treating conditions related to
PT   inappropriate vascularization and angiogenesis
XX
PS   Claim 1; Page 164-165; 180pp; English.
XX
CC   The patent discloses novel polypeptides critical for angiogenesis and
CC   vascularisation and nucleic acids encoding them. The sequences of the
CC   present invention are used in the prevention, treatment and diagnosis
CC   of diseases associated with inappropriate angiogenesis and/or neo- or
CC   cardiovascularisation. They are used in the diagnosis, prevention
CC   or treatment of angiogenic disorders such as cardiac hypertrophy,
CC   congestive heart failure (CHF), myocardial infarction, aortic stenosis,
CC   vascular restenosis and vascular trauma such as wounds, burns or
CC   surgery. They are also used in the treatment of cancer and endothelial
CC   diseases. The proteins of the invention are used as antigens in the
CC   production of antibodies against the angiogenesis and vascularisation
CC   proteins and in assays to identify modulators (agonists and antagonists)
CC   of their expression and activity. The antibodies and antagonists are
CC   used to down-regulate expression and activity of the protein of the
CC   invention. The antibodies are also used as diagnostic agents for
CC   detecting the presence of the proteins of the invention in samples.
CC   The sequences of the invention are also used as vaccines and in gene
CC   therapy. The present sequence is novel human PRO-C MG.2 protein
CC   which is encoded by DNA C MG.2 1776 cDNA clone of the invention.
XX
SQ   Sequence   577 AA;

  Query Match             100.0%;  Score 3001;  DB 22;  Length 577;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-229;
  Matches  577;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MATMEKPPAQKVLLDDTVPLTAAIEASQSLQSHTEYIIRVQRGISVENSWQIVRRYSDFD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 matmekppaqkvllddtvpltaaieasqslqshteyiirvqrgisvenswqivrrysdfd 60

Qy         61 LLNNSLQIAQLSLPLPPKKLIGNMDREFIAERQKGLQNYLNVITTNHILSNCELVKKFLD 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 llnnslqiaqlslplppkkligndrefiaerqkglqnylnvittnhilsncelvkkfld 120

Qy        121 PNNYSANYTEIALQQVSMTTRSEPKWEVVEPLKDLWRIRKKYTLMKIKRQPKEEEIVLSW 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 pnnysanyteialqqvsmttrsepkwevveplkdlwrirkkytlmkikrqpkeeeivlsw 180

Qy        181 ADLGPDKYLSDKDFQELIKLLPSCLHPYIYRVTTATANESSALLIRMTNEKQTLKDIIYK 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 adlgpdkylsdkdfqelikllpsclhpyiyrvttatanessallirmtnekqtlkdiiyk 240

Qy        241 AKPKDPPLKKYCNPEKIQELEIQQIPIYCFQTLEVLKKLHDKGFPYGHLHASNVMLDGDT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 akpkdpplkkycnpekiqeleiqqipiycfqtlevlkklhdkgfpyghlhasnvmldgdt 300

Qy        301 CRLLDLENSLLGLPSFYRSYFSQFRKINTLESVDVHCFGHLLYEMTYGRPPDSVPVDSFP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 crlldlensllglpsfyrsyfsqfrkintlesvdvhcfghllyemtygrppdsvpvdsfp 360

Qy        361 PAPSMAVVAVLESTLSCEACKNCMPTISRLLQMPLFSDVLLTTSEKPQFKIPTKLKEALR 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 papsmavvavlestlsceackncmptisrllqmplfsdvllttsekpqfkiptklkealr 420

Qy        421 IAKEQLEKKLLEQKQLHQHRRLIEAQCHRREILEEEKRRLTAKKKTERRGALENSEEHSA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 iakeqlekklleqkqlhqhrrlieaqchrreileeekrrltakkkterrgalenseehsa 480

Qy        481 RYSNSNNSGSGASSPLTSPSSPTPPSTSGISALPPPPPPPPPPAAPLPPASTEVPAQLSS 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 rysnsnnsgsgassspltspssptppstsgisalpppppppppaaplppastevpaqlss 540

Qy        541 QAVNGMSRGALLSSIQNFQKCTLRKAKTEDHSAPKIG 577
              |||||||||||||||||||||||||||||||||||||
Db        541 qavngmsrgallssiqnfqkctlrkaktedhsapkig 577


RESULT     2
AAB65680
ID   AAB65680 standard; Protein; 649 AA.
XX
AC   AAB65680;
XX
DT   27-MAR-2001  (first entry)
XX
DE   Novel protein kinase, SEQ ID NO: 208.
XX
KW   Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
KW   immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;
KW   dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
KW   immune disorder; cardiovascular disease; neurodegenerative disease;
KW   cancer; autoimmune disorder; stroke; inflammatory bowel disease;
KW   inflammatory pelvic disease; multiple sclerosis; psoriasis.
XX
OS   Homo sapiens.
XX
PN   WO200073469-A2.
XX
PD   07-DEC-2000.
XX
PF   26-MAY-2000; 2000WO-US14842.
XX
PR   28-MAY-1999;   99US-0136503.
XX
```

```
PA   (SUGE-) SUGEN INC.
XX
PI   Plowman GD, Martinez R, Whyte D, Sudarsanam S;
XX
DR   WPI; 2001-[illegible]/[illegible].
DR   N-PSDB; AAF41[illegible]08.
XX
PT   Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT   treating immune-related diseases and disorders, cardiovascular disease,
PT   neurodegenerative diseases and/or cancers -
XX
PS   Claim [illegible]; Fig [illegible]; [illegible]pp; English.
XX
CC   The present sequence is a novel protein kinase. The novel protein kinases
CC   and the nucleic acids that encode them may be used in the treatment and
CC   diagnosis of diseases associated with inappropriate kinase expression
CC   such as immune-related diseases and disorders, cardiovascular disease,
CC   neurodegenerative diseases and/or cancers. The nucleic acids and
CC   complementary sequences may also be used as DNA probes in diagnostic
CC   assays. The kinase polypeptides may be used as antigens in the production
CC   of antibodies of kinase expression and activity. Anti-kinase antibodies
CC   and kinase antagonists may also be used to down regulate kinase
CC   expression and activity. Diseases related to kinase expression and
CC   activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC   disorders, complications of organ transplantation, myocardial infarction,
CC   immune disorders, cardiomyopathies, strokes, renal failure,
CC   oxidative stress related disorders, chronic inflammatory bowel disease,
CC   chronic inflammatory pelvic disease, multiple sclerosis, asthma,
CC   osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and
CC   reproductive disorders.
XX
SQ   Sequence [illegible] AA;

  Query Match             [illegible]7.3%;  Score 2919.5;  DB 22;  Length 649;
  Best Local Similarity   [illegible].3%;  Pred. No. 1.5e-222;
  Matches  5[illegible]7;  Conservative    [illegible];  Mismatches    6;  Indels   13;  Gaps    2;

Qy          1 MA[illegible]MEKP[illegible]AKKV[illegible]VVFLLAAIFASQSLQSHTEYIIRVQKGISVENSWQIVRRYSDFD 60
Db          1 matmekpp[illegible]akv[illegible]lqsht[illegible]yiirv[illegible]gis[illegible]w[illegible]ivrrysdfd 60

Qy         61 [illegible]LNN[illegible]NML[illegible]LVKKF[illegible] 120
Db         61 [illegible]lnnslqilalsip[illegible]ppkk[illegible]lsn[illegible]kktld 120

Qy        121 [illegible]EWLVV[illegible]KEFLV[illegible]W 180
Db        121 [illegible] 180

Qy        181 [illegible]YIYEVIIAIANESAI[illegible]EMFN[illegible]LRDLIYK 240
Db        181 [illegible]k 240

Qy        241 AK[illegible]KKY[illegible]HLHASNVMLDCDT 300
Db        241 [illegible]hlhasnvmldcdt 300

Qy        301 [illegible]LENSLIGLPS[illegible]ANCLESV[illegible]LYEMIYC[illegible]PVPVLSFP 360
Db        301 [illegible]dlenslig[illegible]styrs[illegible] 360

Qy        361 [illegible]MAV[illegible]KEKLELAIK 420
Db        361 [illegible] 420

Qy        421 [illegible]LAFFK[illegible]ALLNS[illegible]HFA 480
Db        421 [illegible] 480

Qy        481 [illegible]AAP[illegible]ASTEVPAQLS 540
Db        481 kvs[illegible]sqlsalppppppppppaaplppasteapaqls 540

Qy        541 [illegible]QAVNQMSRCALLSSIQNPQKCTLKKAE [illegible]DHSAPK[illegible] 57[illegible]
Db        541 [illegible]qavnqmsrcallssiq[illegible]pqkct[illegible]kk[illegible] 5[illegible]

RESULT 3
ABB59495
ID   ABB59495 standard; Protein; 563 AA.
XX
AC   ABB59495;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster polypeptide SEQ ID NO 5277.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC, Adams M, Li PWD, Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   N-PSDB; ABL03598.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Disclosure; SEQ ID NO 5277; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL[illegible] ABL[illegible]), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence   563 AA;

  Query Match             29.1%;  Score 874;  DB 22;  Length 563;
  Best Local Similarity   36.2%;  Pred. No. 1.2e-[illegible];
  Matches  295;  Conservative  [illegible];  Mismatches  [illegible];  Indels   84;  Gaps   11;

Qy         84 [illegible]VCMEFRSE 143
Db          [illegible] [illegible]

Qy        144 EWLVVEFLEDLLWEIFKEEYLMKIKNQPKES[illegible] 175
Db          [illegible] [illegible]

Qy        176 [illegible]LVLSWADLGHEKYLS[illegible]YIYEVIIAIANELLA 222
Db        11[illegible] hsidaatldpqsevvaewleyqpdk[illegible]aantenae 178
```

```
Qy    225 [illegible]MENEK[illegible]IYKAK[illegible]NPKKI[illegible]VIKELHD 281
          [illegible]
Db    179 [illegible]kthktt[illegible]kdvlemaanpkntlskyqnpkqrtaismkqvatyqkqi[illegible]alitlhs 238

Qy    282 KGEPY[illegible]HLHASNVML[illegible]RLLDLENSLD[illegible]LPSFYRSYFSQFRKINTLFSVDVHCFGHL 341
          [illegible]
Db    239 k[illegible]yhlhsan[illegible]dk[illegible]l[illegible]tyrp[illegible]qhsk[illegible]tqh 298

Qy    342 LYEMLYGR[illegible]VPVDSFPPAPSMAVVAVLESILSCEACKNGMPTISRLLQMPLFSDVLL 401
          [illegible]
Db    299 [illegible]meyp[illegible]qes[illegible]p[illegible] 357

Qy    402 [illegible]EKPQEK[illegible]EA[illegible]EKEILLQKLIHQHPS[illegible]EA[illegible] 454
          [illegible]
Db    358 [illegible]aekpytklslnakellkqaeiksenrlrdeqksvkpqkr[illegible]qelmessee 417

Qy    455 EKKKPK[illegible]ARKKSKPSALENS      EEHSARYSNSNNSGSGASSPLT---  ------S 498
          [illegible]
Db    418 ekrksk[illegible]pkk[illegible]ssttvqe[illegible] 477

Qy    499 [illegible]SALPPPPPP               PPPPAAPLPPASTEVPAQLSSQAVNG-- 545
          [illegible]
Db    478 d[illegible]ppl[illegible]paphlasiyqqelpsttqapeerqse-tpem[illegible] 536

Qy    5[illegible] MQ[illegible]NL[illegible]KAK[illegible]
          [illegible]
Db    5[illegible] [illegible]krvrand 563


RESULT 4
AAB[illegible]
ID   AAB[illegible] standard; Protein; 155 AA.
XX
AC   AAB[illegible];
XX
DT   [illegible] FEB 2[illegible] (first entry)
XX
DE   Human secreted protein BLAST search protein SEQ ID No: [illegible]36.
XX
KW   [illegible]; immunosuppressive; nootropic; neuroprotective; antiviral;
KW   antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW   [illegible]; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW   [illegible]; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW   [illegible] disease; infection; human; secreted protein.
XX
OS   Homo sapiens.
XX
PN   WO200[illegible]-A1.
XX
PD   [illegible] 200[illegible].
XX
PF   22-MAR-2000; 2000WO-US07483.
XX
PR   2[illegible]-MAR-[illegible];   [illegible]US-0126596.
PR   [illegible]
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   [illegible] CA, [illegible] CM, Komatsoulis G;
XX
DR   WPI; 200[illegible]/[illegible].
XX
PT   Nucleic acid molecules encoding human secreted proteins, used in
PT   preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
PT   Parkinson's diseases and cancers
XX
PS   Disclosure; Page 395-396; 423pp; English.
XX
CC   The invention relates to the isolation of genes AAC66410-C66458 encoding
CC   the human secreted proteins AAB32002-B320[illegible]. This sequence represents a
CC   fragment of the protein encoded by the gene given in the descriptor
CC   line. The sequence is used as a query sequence for doing BLASTX searches
CC   to determine homologous sequence to the protein. The genes and proteins
CC   are useful for preventing, ameliorating or treating medical conditions,
CC   e.g. by protein or gene therapy. The genes are isolated from a range of
CC   human tissues disclosed in the specification. The nucleic acids,
CC   proteins, antibodies and (ant)agonists are useful in the diagnosis,
CC   treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer,
CC   and other cancers of the adrenal gland, bone, bone marrow, breast,
CC   gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders
CC   e.g. Addison's disease, allergies, autoimmune haemolytic anaemia,
CC   autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple
CC   sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC   cardiovascular disorders such as myocardial ischaemias; (d) wound
CC   healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and
CC   (f) infectious diseases such as viral, bacterial, fungal and parasitic
CC   infections.
XX
SQ   Sequence   155 AA;

  Query Match             27.5%;  Score 826;  DB 21;  Length 155;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-57;
  Matches  155;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    195 QCLIKLLPSCLHPYIYKVIFA[illegible]ANESSALLIEMENEKIIIKDLIYKAKPKDPLAKYCNP 254
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 qclikllpsclhpyiykvifa[illegible]kkycnp 60

Qy    255 KKIQ[illegible]ELQQIKTYQRQILEVLKEIHDKQEPYGHLHASNVMLDGDTCRLLDLENSLGLP 314
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 kkiqqlelqqikty[illegible]dqdtcrlldlenslglp 120

Qy    315 SFYRSYFSQFRKINTLESVDVHCFGHLLYEMLYGR 349
          |||||||||||||||||||||||||||||||||||
Db    121 sfyrsyfsqfrkintlesvdvhcfghllyemlygr 155


RESULT 5
AAU17470
ID   AAU17470 standard; Protein; 141 AA.
XX
AC   AAU17470;
XX
DT   07-NOV-2001  (first entry)
XX
DE   Novel signal transduction pathway protein, Seq ID 1035.
XX
KW   Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
KW   antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;
KW   immune system disorder; rheumatoid arthritis; inflammatory condition;
KW   organ transplant rejection; infection; hepatitis C; blood disorder;
KW   sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
KW   neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW   chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
KW   cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
KW   reproductive system; gastrointestinal; liver disorder; AIDS;
KW   acquired immune deficiency syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200154733-A1.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US01312.
XX
PR   31-JAN-2000; 2000US-0179065.
PR   04-FEB-2000; 2000US-0180628.
PR   24-FEB-2000; 2000US-0184664.
PR   02-MAR-2000; 2000US-0186350.
PR   16-MAR-2000; 2000US-0189874.
PR   17-MAR-2000; 2000US-0190076.
PR   18-APR-2000; 2000US-0198123.
PR   19-MAY-2000; 2000US-0205515.
```

PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246542.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250491.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-465460/50.
DR N-PSDB; AAS27387.
XX
PT Novel polypeptides useful for diagnosing, treating, preventing and/or
PT prognosing disorders related to the proteins, including cancers, immune
PT disorders and neuronal disorders
XX
PS Claim 1; SEQ ID No 1035; 880pp; English.
XX
CC The invention relates to novel isolated polypeptides (I), and
CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
CC diagnosing, preventing and treating diseases including immune system
CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune

CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
CC transplant rejections and graft versus host disease, infectious diseases
CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
CC other blood related disorders (sickle cell anaemia), myeloproliferative
CC disorders, primary haematopoietic disorders, hyperproliferative
CC disorders (e.g. Gaucher's disease and cancer), neurodegenerative
CC disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal
CC abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal
CC disorders (e.g. glomerulonephritis), cardiovascular disorders
CC (e.g. arrhythmia), respiratory disorders, dermatological disorders, in
CC wound healing, epithelial cell proliferation, endocrine disorders (e.g.
CC Addison's disease), reproductive system disorders, gastrointestinal
CC disorder (inflammatory disorders), liver disorders (cirrhosis),
CC as stimulators of B cell responsiveness to pathogens, activators of
CC T cells, to induce higher affinity antibodies, and as a means to induce
CC tumour proliferation in pathologies e.g. acquired immune deficiency
CC syndrome (AIDS). AAU17059-AAU17683 represent novel signal transduction
CC pathway proteins, amino acid sequences of the invention.
XX

```
  Query Match             13.[illegible]%;  Score [illegible];  DB 22;  Length 141;
  Best Local Similarity   95.8%;  Pred. No. 8.4e-38;
  Matches  [illegible];  Conservative  [illegible];  Mismatches  [illegible];  Indels  0;  Gaps  0;

Qy        1 [illegible] 60
Db        9 [illegible]maitmekppaqkv[illegible]rysdld 68

Qy       61 [illegible]NNSLQ[illegible] 118
Db       69 [illegible]qarlslpippkkliqnmdretiaerqkqlqnylnvittnhilsnedwlxst 126
```

RESULT [illegible]
ABB[illegible]
ID ABB[illegible] standard; Protein; 515 AA.
XX
AC ABB[illegible];
XX
DT [illegible]-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 14781.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; [illegible].
DR N-PSDB; ABL0[illegible].
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.
XX
PS Claim [illegible]; SEQ ID NO 14781; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16126-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 515 AA;

```
  Query Match             13.1%;  Score 392.5;  DB 22;  Length 515;
  Best Local Similarity   30.3%;  Pred. No. 1.4e-22;
  Matches  122;  Conservative  58;  Mismatches  125;  Indels  97;  Gaps  13;

Qy      145 FW[illegible]VV[illegible]KYLSDKDFQ 195
Db      174 ryevlahldelqrhqknwl[illegible]lplppd[illegible]atedlppnecar[illegible]e 229

Qy      196 [illegible]FAYANL[illegible]YFAHFL[illegible]Y 251
Db      230 ilmelqslhhpyiyp[illegible]pwrky 289

Qy      252 [illegible]NSL 310
Db      290 --trkpnqlp[illegible]lsqlenal 347

Qy      311 [illegible]MAVV 368
Db      348 lqlssrinavmws rsvtelenvdivetqhllyemet[illegible]pkpsmavlem 399

Qy      369 -- ------ - -AVLEST-LSCEACKNCMFLISKLLQMPLESDVLLISEKPQEKIPTK 414
Db      400 elqhypqiqqtrkqileilqllteppsqvepsvedlvledllrsidlrelrqpet-- st 456

Qy      415 LKEALRIAKE[illegible]LAKKKSKRSALEN 474
Db      457 ikpsl-------------------- ---- -- ----- srstlnllqavkkrqea 478

Qy      475 SEEHSARYSNSNNSGSGASSPLTSPSSPTPPSTSGISALPPP 516
Db      479 ---------slqhslseanspetppstphdrrt---qvlpap 508
```

RESULT 7
ABB62672
ID ABB62672 standard; Protein; 515 AA.
XX
AC ABB62672;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 14808.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX

```
DR   WPI; 2001-076860/75.
DR   N-PSDB; ABL36775.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Disclosure; SEQ ID No 148.8; 2ipp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL16475-ABL16775) and the encoded proteins
CC   (ABB67770-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   515 AA;

  Query Match             12.1%;  Score 392.5;  DB 22;  Length 515;
  Best Local Similarity   30.3%;  Pred. No. 1.4e-22;
  Matches  122;  Conservative   58;  Mismatches  125;  Indels   97;  Gaps   13;

Qy        145 FWFVVEF FEFWs ISFF IMF NQFKEL            VII WAEI KYLSDKDFQ 195
Db        174 ryeviahidoiqsrhqkrwtlrtdasvrtdrlatllplppdevatedlppneear    e 229

Qy        196 CLIKLLPSCLHPYIYRVT---FATANESSALLIRMENEKGTLKDLIYKAKPKDPFLKKY 251
Db        230 eimeilqslhhpyiypvldlqtlrnssyryarlvtpfnsrqsikdliykaqwnepwarky 289

Qy        252 YNFEKIQ  LE QI KTY  R ILEV KF  F   E  Y  HA NVMLD  ICRLLDLENSL 310
Db        290 --trkpnqlpvsqvqrlqrqilealtflkerqtplhqlhsqnvilqnqaarlsqlenql 347

Qy        311 LGLPSFYRSYFSQFRKINL  SVDVHCFGHL YEMIYGRPPDSVPVDSFPPAPSMAVV-  368
Db        348 lqlssrinavmws rsvteienvdivetqhllyemstqq------e ttpkpsmrvlem 399

Qy        369 --           AVLESI  ACEACKNCMPTISRILQMP FSDVLL  SEAIQEKIPTK 414
Db        400 elqhypqiqtrkqileilqlitepppsqvepsvedlvredltrsidlreirqpef---st 456

Qy        415 LFFAIR                  IPGHPF  SVA HBE  LSKKEEKILAKKSKRSALEN 474
Db        457 ikpsl-                              ---------srstlnlqavkkrqea--- 478

Qy        475 SEEBSAKYSNSNNS SGASSPI ISESSPTLPSLSSISALPPP 516
Db        479    -- -siqhs seanspetppstphtrrt---qvipap 508


RESULT   8
AAB32077
ID   AAB32077 standard; Protein; 157 AA.
XX
AC   AAB32077;
XX
DT   14-FEB-2001  (first entry)
XX
DE   Human secreted protein BLAST search protein SEQ ID NO: 135.
XX
KW   Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
KW   antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
KW   vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic;
KW   cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW   neurological disease; infection; human; secreted protein.
XX
OS   Homo sapiens.
XX
PN   WO200058350-A1.
XX
PD   05-OCT-2000.
XX
PF   22-MAR-2000; 2000WO-US07483.
XX
PR   26-MAR-1999;   99US-0126596.
PR   22-DEC-1999;   99US-0171552.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM,  Komatsoulis G;
XX
DR   WPI; 2000-602357/57.
XX
PT   Nucleic acid molecules encoding human secreted proteins, used in
PT   preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
PT   Parkinson's diseases and cancers
XX
PS   Disclosure; Page 394-395; 423pp; English.
XX
CC   The invention relates to the isolation of genes AAC66410-C66458 encoding
CC   the human secreted proteins AAB32041-B3205. This sequence represents a
CC   peptide fragment homologous to the protein encoded by the gene given
CC   in the descriptor line. The sequence is a search result from a BLASTX
CC   homology search. The genes and proteins are useful for preventing,
CC   ameliorating or treating medical conditions, e.g. by protein or gene
CC   therapy. The genes are isolated from a range of human tissues disclosed
CC   in the specification. The nucleic acids, proteins, antibodies and
CC   (ant)agonists are useful in the diagnosis, treatment and prevention of:
CC   (a) cancer, e.g. breast and ovarian cancer, and other cancers of the
CC   adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
CC   lung, or urogenital; (b) immune disorders e.g. Addison's disease,
CC   allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC   diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC   arthritis and ulcerative colitis; (c) cardiovascular disorders such
CC   as myocardial ischaemias; (d) wound healing; (e) neurological diseases
CC   e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such
CC   as viral, bacterial, fungal and parasitic infections.
XX
SQ   Sequence   157 AA;

  Query Match             11.1%;  Score 332;  DB 21;  Length 157;
  Best Local Similarity   45.6%;  Pred. No. 1.7e-14;
  Matches   73;  Conservative   28;  Mismatches   51;  Indels    8;  Gaps    4;

Qy        195 QCLIKLLPSCLHPYIYRV----FATANESSALLIRMENEKGTLKDLIYKAKPKDPFLKK 250
Db          1 eilmellqslhhpyiypvldlqtlrnssyryarlvtpfnsrqsikdliykaqwnepwark 60

Qy        251 YCNPEKIQGLEKQQIKTYCRQILEVLKFLHEKGFPYGHLHASNVMLDGDICRLLDLENS 309
Db         61 y--trkpnqlpvsqvqrlqrqilealtflkerqtplhqlhsqnvilqnqaarlsqlenq 118

Qy        310 LLGLPSFYRSYFSQFRKINTLESVDVHCFGHLLYEMIYGR 349
Db        119 llqlssrinavmws-rsvteienvdivetqhllyemstqq 157


RESULT   9
AAM38834
ID   AAM38834 standard; Protein; 496 AA.
XX
AC   AAM38834;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polypeptide SEQ ID NO 1979.
XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
```

```
KW   peripheral nervous system, neuropathy, central nervous system, CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy Drager Syndrome, chemotactic,
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US34263.
XX
PR   21-JAN-2000; 2000US-0488725.
PR   25-APR-2000; 2000US-0552317.
PR   09-JUN-2000; 2000US-0598042.
PR   19-JUL-2000; 2000US-0620312.
PR   03-AUG-2000; 2000US-0653450.
PR   14-SEP-2000; 2000US-0662191.
PR   19-OCT-2000; 2000US-0693036.
PR   29-NOV-2000; 2000US-0727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI   Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI   Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   N-PSDB; AAI5[illegible].
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders
PT   such as central nervous system injuries
XX
PS   Example 3; SEQ ID NO 1979; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC   the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: immune system suppression,
CC   activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   receptor/receptor activity, arthritis and inflammation, leukaemias and
CC   CNS disorders.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification.
XX
SQ   Sequence 496 AA.

  Query Match             7.1%;  Score 212.5;  DB 22;  Length 496;
  Best Local Similarity   21.4%;  Pred. No. 2.4e-08;
  Matches   [illegible];  Conservative   85;  Mismatches  179;  Indels   93;  Gaps   19;

Qy         27 IVELIAAILAQSEQGHIEYIIRVQ[illegible]GSVENGWQIVRRYSDFDLLNNSL  QIAGLSLP 74
Db         2[illegible] [illegible]kkkr[illegible]ykel[illegible]  rsqwl[illegible]ry[illegible]dklyn[illegible]kkqtpamalk 71

Qy         75 LPPKKL[illegible]NMEREFIAERQKGLQNYLNVI[illegible]NHLLSN[illegible]ELVKKFL          [illegible] 120
Db         7[illegible] [illegible]pdet[illegible]pdt[illegible]kq[illegible]q[illegible]lp[illegible]ypelyn[illegible]pdvratlpmdepkhqsdpsed 131

Qy        121 FNNYSANYIFIAQQVSMEFRGEI  EWEVVLEGLE[illegible]            WKLKKEYILMK 167
Db        132 [illegible]pkl[illegible]qnin[illegible]qpsqmphakpt[illegible]dl[illegible]kv[illegible]qkqstqkv[illegible]ak[illegible]k[illegible]qktyrek 191

Qy        168 IKNQPEEKLVLSWA[illegible]GPEKYLSFKF[illegible]Q[illegible]LIKLLLSCLHPYIYRVIFAIANESSALLIRM 227
Db        192 [illegible]l     qkkivlarke  qkhir[illegible]erne       [illegible]k[illegible]kpt[illegible]qlly[illegible]q[illegible]k[illegible]y[illegible]ld 241

Qy        229 FNEKGIKELLYKAKPKIPFLKKYCNPKKIQGLLIQQIKIYGPQILEVLKFLHPKGFPYG 287
Db        242 fqyqqel ------ --    tthlqrerstpehrartyaaeiasalqylhsikivyr 285

Qy        288 HLHASNVMLDG          DFCK     LLELENSLIGLPSFYRSYFSQFRKINILESVD 334
Db        286 dlkpenilldsqghvvltdfglckeqiaisdt[illegible]tfcgtpeylap  evlrkqpydntvd 343

Qy        335 VHCFGHLLYEMIYGRPP               DSV     PVDSFPPAPSMAVVAVLESILSCEACK 381
Db        344 wwclgavlyemlyglppfyerdvaemydnilhkpl-slrpavslfawsileellekdr q 401

Qy        382 NGMPTISRLLQM---PLFSDVLLTTSEKPQFKIP 412
Db        402 nrlgake[illegible]fl[illegible]iqnhpffes  lswadl[illegible]qkkip 433
```

```
RESULT 10
AAM40620
ID   AAM40620 standard; Protein; 496 AA.
XX
AC   AAM40620;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polypeptide SEQ ID NO 5551.
XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system, neuropathy, central nervous system, CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy Drager Syndrome, chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US34263.
XX
PR   21-JAN-2000; 2000US-0488725.
PR   25-APR-2000; 2000US-0552317.
PR   09-JUN-2000; 2000US-0598042.
PR   19-JUL-2000; 2000US-0620312.
PR   03-AUG-2000; 2000US-0653450.
PR   14-SEP-2000; 2000US-0662191.
PR   19-OCT-2000; 2000US-0693036.
PR   29-NOV-2000; 2000US-0727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI   Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI   Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   N-PSDB; AAI59776.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders
PT   such as central nervous system injuries -
XX
PS   Example 2; SEQ ID NO 5551; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC   the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
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CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   [illegible] activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification.
XX
SQ   Sequence   496 AA;

  Query Match             7.[illegible]%;  Score [illegible].5;  DB 22;  Length 496;
  Best Local Similarity   21.4%;  Pred. No. 2.8e-08;
  Matches   97;  Conservative   85;  Mismatches  179;  Indels   93;  Gaps   19;

Qy         17 TVPLTAAIEASQSLQSHIFYIIRVQRGISVENSWQIVRRYSDFDLLNNSL--QIACLSLP 74
Db         15 svsipssdehrokkkr[illegible] 71

Qy         75 LPPKKLI[illegible]NMDFEFIAERQKGLQNYLNVITTNHILSNCELVKKFL            D 120
Db         72 ipakriitqdntdpdtikqrraqlnetiqqlvrypelynhpdvratlqmdspkhqsdpsed 131

Qy        121 PNNYSANYTEIALQQVSMFFRSDP  KWEVVEILKDI[illegible]-----------WRIRKKYFLMK 167
Db        132 ederssqk[illegible] 191

Qy        168 IKNQPKERLVLSWADLCPDKYLSDKDPQ[illegible]IKIIPSCLHPYIYPVTFATANESSALIIRM 227
Db        192 vl---qkkivlerko--qkhimqerr[illegible]---llknekhpl[illegible]teklytvld 241

Qy        228 FNEEGILEDLIYEAKPEDPELEEY[illegible]NPEEIQCLELQQIKTYCRQILEVLKEPLHEKGFPYG 287
Db        242 fvnqqel   ---  ---------  tthlqrerstpehrartyaaeiasalcylhsikivyr 285

Qy        288 HLHASNVMLDG     -   ---  DTCR  -  LLDLENSLLGLPSFYRSYFSQFRKINTLESVD 334
Db        286 dlkpen[illegible]lldsvghvvltdfglckeqiaisdtttttfcgtpeylap  evlrkqpydntvd 343

Qy        335 VHCFGHILYEMTYGRPP--          -DSV--PVDSFPPAPSMAVVAVLESTLSCEACK 381
Db        344 wwclqav[illegible]yemlyqlppfyer[illegible]vaemydniihkpl-slrpqvsltawsilqellekdr-q 401

Qy        382 NGMPLISKLLQM --PLFSDVILLISEKPQFKIP 412
Db        4[illegible] [illegible]akedtleiqnnp[illegible]fes--lswadlvqkkip 433


RESULT 11
AAW87772
ID   AAW87772 standard; Protein; 496 AA.
XX
AC   AAW87772;
XX
DT   17 MAR 1999  (first entry)
XX
DE   Human serum glucocorticoid regulated kinase (H-SGK2) polypeptide.
XX
KW   Serum glucocorticoid-regulated kinase; H-SGK2; human; gene therapy;
KW   serine/threonine protein kinase; inflammation; rheumatoid arthritis;
KW   septicaemia; autoimmune disease; inflammatory bowel disease, psoriasis,
KW   transplant rejection; infection; stroke; ischaemia; renal disorder;
KW   restenosis; brain injury; acquired immune deficiency syndrome, AIDS,
KW   metabolic; bone; osteoporosis; lymphoproliferation; atherosclerosis;
KW   Alzheimer's disease; cancer.
XX
OS   Homo sapiens.
XX
PN   EP889127-A1.
XX
PD   07-JAN-1999.
XX
PF   18-JUN-1998;   98EP-0304830.
XX
PR   22-DEC-1997;   97US-0997212.
PR   01-JUL-1997;   97US-0051446.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Kumar S,  Zou C;
XX
DR   WPI; 1999-062658/06.
DR   N-PSDB; AAV99653.
XX
PT   New nucleic acid encoding human H-SGK2 polypeptide(s) - useful for
PT   diagnosis, treatment and prevention of e.g. arthritis, infections,
PT   cancer, Alzheimer's disease
XX
PS   Claim 11; Page 8; 27pp; English.
XX
CC   This represents a human serum glucocorticoid regulated kinase (H-SGK2)
CC   polypeptide, a novel member of the serine/threonine protein kinase
CC   family. A host cell transfected or transformed with an expression system
CC   comprising the H-SGK2 nucleic acid can be used for the recombinant
CC   production of the protein. The H-SGK2 polypeptide is useful for treating
CC   a subject who require enhanced/reduced activity or expression/inhibition
CC   of the polypeptide. Recombinant H-SGK2 is used to raise antibodies; in
CC   vaccines; in drug screens; and to identify soluble or membrane-bound
CC   receptors. The H-SGK2 polypeptide [illegible] inflammation
CC   (rheumatoid arthritis); septicaemia; autoimmune disease (inflammatory
CC   bowel disease or psoriasis); transplant [illegible] stroke;
CC   ischaemia; renal disorders; restenosis; brain injury; acquired immune
CC   deficiency syndrome; metabolic and other bone diseases (osteoporosis);
CC   cancer (e.g. lymphoproliferation); atherosclerosis and Alzheimer's
CC   disease. The H-SGK2 nucleic acid can be used in gene therapy
XX
SQ   Sequence   496 AA;

  Query Match             6.8%;  Score 2[illegible].5;  DB 20;  Length 496;
  Best Local Similarity   21.1%;  Pred. No. 8.4e-08;
  Matches   96;  Conservative   85;  Mismatches  1[illegible];  Indels   93;  Gaps   19;

Qy         17 TVPLTAAIEASQSLQSHIFYIIRVQRGISVENSWQIVRRYSDFDLLNNSL--QIACLSLP 74
Db         15 svsipssdehrokkkrttvykvlvevq  ---sewtv[illegible]rysef[illegible]klyntlkkqfpamalk 71

Qy         75 LPPKKLI[illegible]NMDFEFIAERQKGLQNYLNVITTNHILSNCELVKKFL---          --  D 120
Db         72 ipakrifqdntdpdtikqrraqlnetiqqlvrypelynhpdvratlqmdspkhqsdpsed 131

Qy        121 PNNYSANYTEIALQQVSMFFRSDP  KWEVVEILKDI[illegible]  -          --WRIRKKYFLMK 167
Db        132 ederssqklhetsqninlqpeqnphakptdtdtlkvqkqevskeilakrkltqktyrek 191

Qy        168 IKNQPKERLVLSWADLCPDKYLSDKDPQ[illegible]IKIIPSCLHPYIYPVTFATANESSALIIRM 227
Db        192 vl---qkkivlerko--qkhimqerr[illegible]---llknekhpflvqlhysfqttekly[illegible]ld 241

Qy        228 FNEEGILEDLIYEAKPEDPELEEY[illegible]NPEEIQCLELQQIKTYCRQILEVLKEPLHEKGFPYG 287
Db        242 fvnqqel -       - - - - -  -tthlqrerstpehrartyaaeiasalqylhsikivyr 285

Qy        288 HLHASNVMLDG      -     DTCR     [illegible]INTLESVD 334
Db        286 dlkpenilldsqghvvltdfglckenialsdtttttfcgtpeylap  evlrkqpydntvd 343

Qy        335 VHCFGHILYEMTYGRPP--- ---   -DSV---PVDSFPPAPSMAVVAVLESTLSCEACK 381
Db        344 wwclqavlyemlyqlppfyerdvaemydniilhkp-slrpqvsltawsilqellekdr-q 401
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Qy    [illegible] NIMPIIGRLLQM    PLFSDVLLITSEKPQFKIP 412
                                  |: ::  | |||
Db    [illegible] [illegible]    lswadlvqkkip 4[illegible]
```

RESULT 12
AAY[illegible]
ID   AAY[illegible] standard; Protein; 912 AA.
XX
AC   AAY[illegible];
XX
DT   [illegible] FEB [illegible] (first entry)
XX
DE   Human GEK2 protein.
XX
KW   Antirheumatic; antiathritic; antiinflammatory; antiallergic; osteopathic;
KW   antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosupressive;
KW   neuroprotective; cardiant; cerebroprotective; cytostatic; antidiabetic;
KW   [illegible] protein kinase; SLK2; [illegible] SLK4; [illegible] SLK7;
KW   [illegible] Z2, Z3, Z4, KHS2, SULU1, SULU3, GEK2, PAK4; PAK5; antagonist;
KW   antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma;
KW   inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
KW   rhinitis; autoimmunity; organ transplantation; multiple sclerosis;
KW   myocardial infarction; cardiovascular disease; stroke; renal failure;
KW   oxidative stress related neurodegenerative disorder; Parkinson's disease;
KW   amylotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;
KW   ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
KW   mesangial disorder; growth regulation; wound healing; T cell activation;
KW   immunosuppressant.
XX
OS   Homo sapiens.
XX
PN   WO9953036-A2.
XX
PD   21-OCT-1999.
XX
PF   [illegible] APR [illegible]; [illegible]
XX
PR   14 APR 1998; [illegible] 0081784.
XX
PA   ([illegible]) [illegible] INC
XX
PI   [illegible] Martinez R, Whyte D;
XX
DR   WPI; [illegible]
DR   N-PSDB; AA[illegible]
XX
PT   Novel kinase related polypeptides used for the diagnosis and treatment
PT   of kinase related diseases and disorders
XX
PS   [illegible] Page [illegible]; 387pp; English.
XX
CC   This sequence represents a novel STE20 related protein kinase. The
CC   invention relates to nucleic acid molecule encoding a kinase polypeptide
CC   selected from SLK2, SLK3, SLK4, SLK5, SLK6, SLK7, Z1, Z2, Z3,
CC   Z4, KHS2, SULU1, SULU3, GEK2, PAK4 and PAK5. The proteins are used to
CC   identify agonists and antagonists, and to raise antibodies. The
CC   polynucleotides are useful in gene therapy protocols. The polynucleotides,
CC   polypeptides, antibodies, antagonists and agonists may be used to treat
CC   diseases such as immune related disorders and diseases (e.g. rheumatoid
CC   arthritis, artherosclerosis, chronic inflammatory bowel disease (e.g.
CC   Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,
CC   rhinitis, autoimmunity, and organ transplantation, chronic inflammatory
CC   pelvic disease, multiple sclerosis, organ transplantation, myocardial
CC   infarction, cardiovascular disease, stroke, renal failure, oxidative
CC   stress related neurodegenerative disorders (e.g. amylotrophic lateral
CC   sclerosis, Parkinson's disease and Leigh syndrome), cancer,
CC   cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes
CC   mellitus, fibrotic and mesangial disorders. The proteins may also be
CC   useful for cell growth regulation (e.g. in wound healing), T cell
CC   activation, mitosis control, and as immunosuppressants
XX
SQ   Sequence 912 AA;

```
  Query Match             6.6%;  Score 199.5;  DB 20;  Length 912;
  Best Local Similarity   24.2%;  Pred. No. 5.8e-07;
  Matches  123;  Conservative   [illegible];  Mismatches  181;  Indels  141;  Gaps   25;

Qy    113 ELVKKFLPPNNYSANY[illegible]EIA[illegible]QVSMEPFSEPKWEVVEPLE[illegible]GWRIRKKYPLMKIKNQP 172
          | |:: ||||                       ||:|  | |      | !   | ||
Db     24 ehvrrdldpnev  -  -       -   -  -wei[illegible]pel[illegible]-[illegible]tqkey   k[illegible]kn   55

Qy    173 KERLVLSWAPLGPDKYLSD KDF[illegible]LIKLL[illegible]CLHPYIYRVIFAIANE[illegible]ALLIRMPNEK 2[illegible]1
          ||    |: |  :     |     : :|:    |::| :| |||| ::    |   ::      ::   |
Db     56 ket[illegible]alaa[illegible]k[illegible]y[illegible]l[illegible]p[illegible]y[illegible]k[illegible] [illegible]yy[illegible]lwimletepa 115

Qy    232 [illegible]ILE[illegible]LL[illegible]AEE[illegible]FL[illegible]EY [illegible]GHLHA 291
          |  :   :: :                  :||    ||:    ||:|| | ||| |     :   | |
Db    116 qavdaimle[illegible]d-  --             [illegible]lt[illegible]p[illegible]v[illegible]q[illegible]l[illegible]lnflhskrilhrdlka 160

Qy    292 [illegible]NVM  [illegible]         [illegible]YE[illegible]NILL        [illegible] 332
           ||:   |:||              : |     :| :| |  :          :      |::
Db    161 qnvlmtleqdirladfqvsaknlktlqkrdsfiqtpywma---pevvmcetmkdtpydyk 217

Qy    333 VDVHCFGHLLYEMTYGRPP  DSVFV           [illegible]SFPP    AFSMAVVAVLESILSCEAC 380
           |:     |   |  ||      ||   :    |:                | ||       ||     |          |
Db    218 [illegible]diwsl[illegible]itl[illegible]emaq[illegible]e[illegible]p[illegible]hhe[illegible]lnpm[illegible]vllkiak[illegible]dpptll[illegible]pskws[illegible] [illegible]fkiald 276

Qy    381 KN--CMP[illegible]SPL[illegible]QMP[illegible]SPVLL[illegible]SFFP[illegible]E[illegible]ALK[illegible]AKE[illegible]EKRLIEEQKQIH 438
          ||       |: ::||:        |  :      || |                |||      :  :  :     |     ::
Db    277 k[illegible]petrpsaaqllehpfvs[illegible]i    [illegible]snk               al:     [illegible]ak[illegible]meeie 319

Qy    439 QHRRLTPAQSPHCSFFFRKKKKILARKKS[illegible]SA[illegible]NSFEHSARYSNSNNSGSGASSPL T 497
             |               | ||:                          | ||    ::|:    |     :          |   ||
Db    320 dqr           deqeed              avdaastlenhtqnasevspps    lnadkplee 360

Qy    498 SPSSPTPPS------------TSGISALPPPPPPPPPP---      AAPLP  -   -PASTEV 534
          |||:|    ||                      ||     :|          ||        |            | |:|           | |  :
Db    361 spstplapsqsqdsvnepcsqpsqdrslqttsppvvapqnenlavpvplrksrpvsmda 420

Qy    535 PAQLSSQAVNGMSRGALLSSIQNFQKGT 562
            |::  :              |  |     :         ||  :
Db    421 riqvaqekqvaeqqqdlspaanr[illegible]qkas 448
```

RESULT 13
AAY55966
ID   AAY55966 standard; Protein; 968 AA.
XX
AC   AAY55966;
XX
DT   18-FEB-2000 (first entry)
XX
DE   Full length human GEK2 protein.
XX
KW   Antirheumatic; antiathritic; antiinflammatory; antiallergic; osteopathic;
KW   antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosupressive;
KW   neuroprotective; cardiant; cerebroprotective; cytostatic; antidiabetic;
KW   vulnery; STE20 protein kinase; SLK2; SLK3; SLK4; SLK5; SLK6; SLK7;
KW   Z1, Z2, Z3, Z4, KHS2, SULU1, SULU3, GEK2, PAK4; PAK5; antagonist;
KW   antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma;
KW   inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
KW   rhinitis; autoimmunity; organ transplantation; multiple sclerosis;
KW   myocardial infarction; cardiovascular disease; stroke; renal failure;
KW   oxidative stress-related neurodegenerative disorder; Parkinson's disease;
KW   amylotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;
KW   ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
KW   mesangial disorder; growth regulation; wound healing; T cell activation;
KW   immunosuppressant.
XX
OS   Homo sapiens.
XX
PN   WO9953036-A2.
XX
PD   21-OCT-1999.

```
XX
PF   1 APR 1999;   99WO-US08150.
XX
PR   14 APR 1998;   98US-0081784
XX
PA   (SUGE ) SUGEN INC.
XX
PI   Plowman G, Martinez R, Whyte D.
XX
DR   WPI; 1999-611301/52.
DR   N-PSDB; AAZ4054.
XX
PT   Novel kinase-related polypeptides used for the diagnosis and treatment
PT   of kinase-related diseases and disorders -
XX
PS   Claim 11; Page 375-378; 537pp; English.
XX
CC   This sequence represents a novel STE20-related protein kinase. The
CC   invention relates to nucleic acid molecule encoding a kinase polypeptide
CC   selected from [illegible]
CC   ZC4, KHS2, SULU1, SULU3, GEK2, PAK4 and PAK5. The proteins are used to
CC   identify agonists and antagonists, and to raise antibodies. The
CC   polynucleotides are useful in gene therapy protocols.The polynucleotides,
CC   polypeptides, antibodies, antagonists and agonists may be used to treat
CC   diseases such as immune-related disorders and diseases (e.g. rheumatoid
CC   arthritis, artherosclerosis, chronic inflammatory bowel disease (e.g.
CC   Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,
CC   rhinitis, autoimmunity, and organ transplantation, chronic inflammatory
CC   pelvic disease, multiple sclerosis, organ transplantation, myocardial
CC   infarction, cardiovascular disease, stroke, renal failure, oxidative
CC   stress related neurodegenerative disorders (e.g. amylotrophic lateral
CC   sclerosis, Parkinson's disease and Leigh syndrome), cancer,
CC   cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes
CC   mellitus, fibrotic and mesangial disorders. The proteins may also be
CC   useful for cell growth regulation (e.g. in wound healing), T cell
CC   activation, mitosis control, and as immunosuppressants.
XX
SQ   Sequence   968 AA

  Query Match              6.6%;  Score 199.5;  DB 20;  Length 968;
  Best Local Similarity   21.2%;  Pred. No. 6.3e-07;
  Matches  12[illegible];  Conservative   66;  Mismatches  134;  Indels  141;  Gaps   25;

Qy    11[illegible] EIVKK[illegible]NNY[illegible]LMKIFNQP 172
Db     24 [illegible]dldpn[illegible] --  -we[illegible]vqelqd--qa[illegible]kvy---kak[illegible]  5[illegible]

Qy    17[illegible] K[illegible]SWA[illegible]PYIVRVTFATAN[illegible]ALLIEMPNEK 2[illegible]
Db     5[illegible] k[illegible]akv[illegible]k[illegible]dyiveieilat[illegible]dhpyivk[illegible]ayyhd[illegible]klwimie[illegible] 11[illegible]

Qy    23[illegible] [illegible]LEK[illegible]FPVV[illegible]HA 29[illegible]
Db    116 [illegible]d--- --------[illegible]lhrdika 16[illegible]

Qy    29[illegible] SNVM [illegible] ---I[illegible]RLLPLENSILGLPSFYRSYFSQFRKINIIF------S 332
Db    16[illegible] [illegible]avsak[illegible] 217

Qy    3[illegible] V[illegible]MI[illegible]SV[illegible] [illegible]----A[illegible]SMAVVAV[illegible]SILSCFA[illegible] 3[illegible]
Db    21[illegible] adlws[illegible]lliem[illegible]dppt[illegible]ltpskws[illegible]rdflkiald 276

Qy    3[illegible] [illegible]FEII[illegible]ELKEALRIAKE[illegible]EEQKCIH 438
Db    27[illegible] k[illegible]alr [illegible]elv[illegible]akaevmeeie 31[illegible]

Qy    4[illegible] [illegible]NCNN[illegible]SCA[illegible] 4[illegible]
Db    3[illegible] [illegible] ---dedeeed---- [illegible]avdaas[illegible]pps [illegible] 3[illegible]

Qy    4[illegible] SPSSPIPPS- -   TSGISALIPPPPLPP-P- ----AAPIP ----PASTPV 5[illegible]
```

```
Db    361 spstplapsqsqdsvnepesqpsqdrs[illegible]qttsppv[illegible]avpv[illegible]rksrpvsmda 420

Qy    5[illegible] [illegible]AV[illegible]NCMS[illegible]CAI[illegible]NR[illegible]K[illegible] 562
Db    421 [illegible]iqvaqekqvaeqqqdlspaan[illegible]sqka[illegible] 44[illegible]

RESULT 14
AAY93499
ID   AAY93499 standard; Protein; 1081 AA.
XX
AC   AAY93499;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Amino acid sequence of the protein kinase Pkh2 polypeptide.
XX
KW   Protein kinase; Pkh1; Pkh2; Ypk1; Yrk2; protein kinase B-alpha;
KW   human serum and glucocorticoid induced protein kinase; SGK; PKBalpha;
KW   3-phosphoinositide-dependent protein kinase 1; PDK1; fungal infection;
KW   thrush; cancer; diabetes; obesity; antifungal; Candida infection.
XX
OS   Saccharomyces cerevisiae.
XX
PN   WO200036135-A2.
XX
PD   22-JUN-2000.
XX
PF   14-DEC-1999;   99WO-GB04228.
XX
PR   14-DEC-1998;   98US-0112114.
XX
PA   (MEDI ) MEDICAL RES COUNCIL.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Thorner JW, Alessi DR, Torrance PD, Casamayor A;
XX
DR   WPI; 2000-442391/38.
DR   N-PSDB; AAA46567.
XX
PT   Screening method identifying compounds which modulate protein kinase
PT   activity for use in treating fungal infections and cancer
XX
PS   Disclosure; Page 17-18; 151pp; English.
XX
CC   The present sequence represents a protein kinase Pkh2. The specification
CC   describes a screening method to identify a compound which modulates the
CC   activity of protein kinases from different sources, using yeast
CC   cells. The method is used to identify a compound which modulates
CC   (inhibits) the activity of a protein kinase, Pkh1 or Pkh2 phosphorylate
CC   and activate Ypk1, Yrk2, human serum and glucocorticoid induced protein
CC   kinase (SGK) or protein kinase B-alpha (PKBalpha). 3-phosphoinositide
CC   dependent protein kinase-1 (PDK1) is used to phosphorylate and activate
CC   Ypk1 and Yrk2 or SGK but not PKBalpha or p70S6 kinase. Compounds
CC   identified by the methods are used to treat fungal infections e.g.
CC   thrush, and to treat cancer. To treat cancer, the compounds inhibit PKB,
CC   PDK1 or the activation of PKB by PDK1. Compounds which activate PKB or
CC   PDK1 can be used in the treatment of diabetes or obesity, and compounds
CC   which inhibit a fungal functional homologue of PDK1 (Pkh1 or Pkh2) or
CC   SGK (Ypk1 or Yrk2) can be used as an antifungal agent to treat Candida
CC   infections, e.g. thrush.
XX
SQ   Sequence   1081 AA;

  Query Match              6.5%;  Score 19[illegible];  DB 21;  Length 1081;
  Best Local Similarity   21.4%;  Pred. No. 1.7e-06;
  Matches  10[illegible];  Conservative   74;  Mismatches  16[illegible];  Indels  144;  Gaps   20;

Qy    16[illegible] [illegible]MK[illegible]VL[illegible]WA[illegible]VRVTFATANES 220
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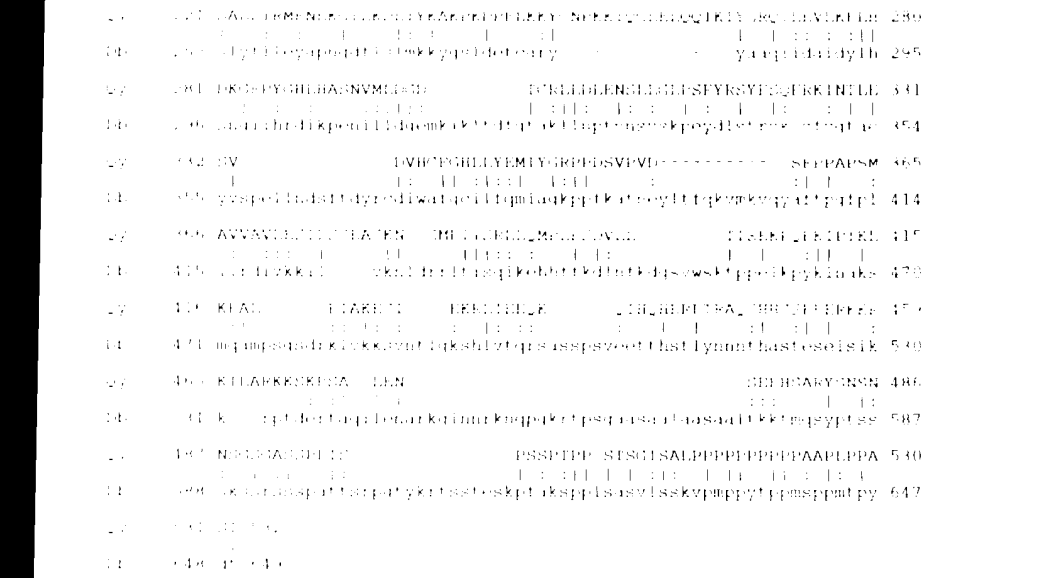
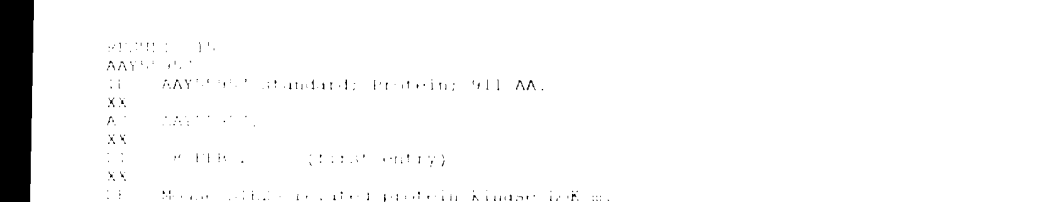
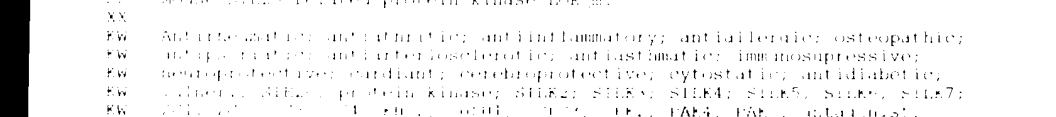
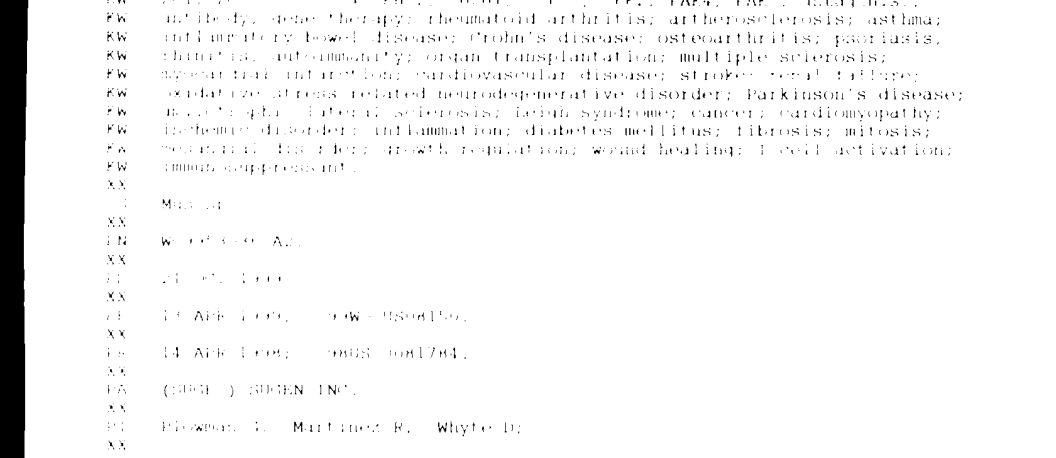






DR WPI; 1999-611301/52.
XX
PT Novel kinase-related polypeptides used for the diagnosis and treatment
PT of kinase related diseases and disorders
XX
PS Disclosure; Page 350 353; 387pp; English.
XX
CC This sequence represents a novel STE20 related protein kinase. The
CC invention relates to nucleic acid molecule encoding a kinase polypeptide
CC selected from STLK2, STLK3, STLK4, STLK5, STLK6, STLK7, ZC1, ZC2, ZC3,
CC ZC4, KHS2, SULU1, SULU3, GEK2, PAK4 and PAK5. The proteins are used to
CC identify agonists and antagonists, and to raise antibodies. The
CC polynucleotides are useful in gene therapy protocols.The polynucleotides,
CC polypeptides, antibodies, antagonists and agonists may be used to treat
CC diseases such as immune-related disorders and diseases (e.g. rheumatoid
CC arthritis, arteriosclerosis, chronic inflammatory bowel disease (e.g.
CC Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,
CC sepsis, autoimmunity, and organ transplantation, chronic inflammatory
CC pelvic disease, multiple sclerosis, organ transplantation, myocardial
CC infarction, cardiovascular disease, stroke, renal failure, oxidative
CC stress-related neurodegenerative disorders (e.g. amyotrophic lateral
CC sclerosis, Parkinson's disease and Leigh syndrome), cancer,
CC cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes
CC mellitus, fibrotic and mesangial disorders. The proteins may also be
CC useful for cell growth regulation (e.g. in wound healing), T cell
CC activation, mitosis control, and as immunosuppressants.
XX
SQ Sequence 911 AA;



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Job time: 124 sec

OM protein - protein search, using sw model

Run on: June 12, 2002, 09:53:49 ; Search time 65.66 Seconds
(without alignments)
214.645 Million cell updates/sec

Title: US-09-684-458-2
Perfect score: 3001
Sequence: 1 MAPMEFFAGKV[illegible]IV[illegible]..........FQKGLPSAKPDHSAFKIG 577

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued_Patents_AA:*
1: [illegible]_COMB.pep:*
2: [illegible]_COMB.pep:*
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4: [illegible]_COMB.pep:*
5: [illegible]_COMB.pep:*
6: [illegible]backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

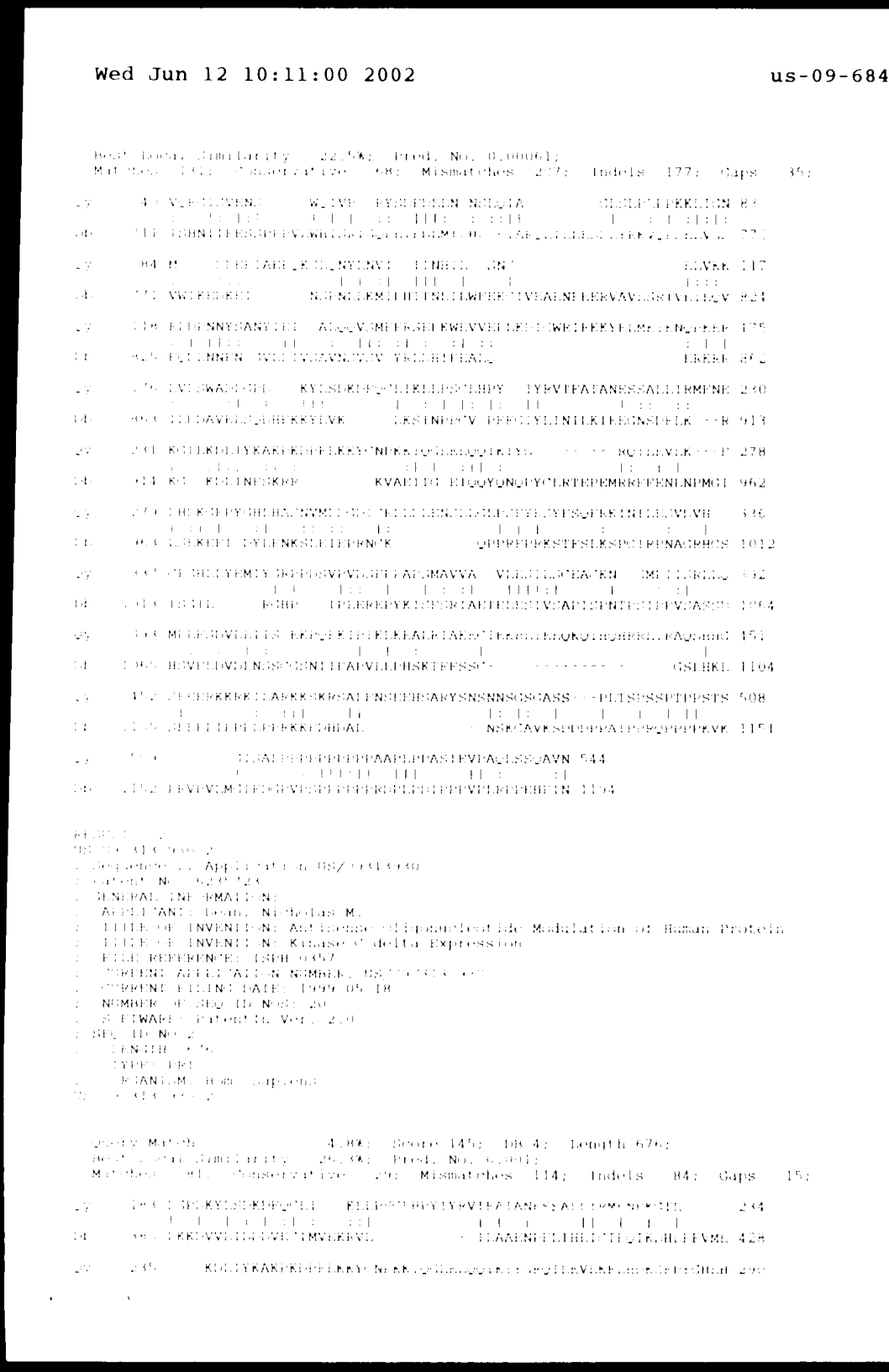
SUMMARIES

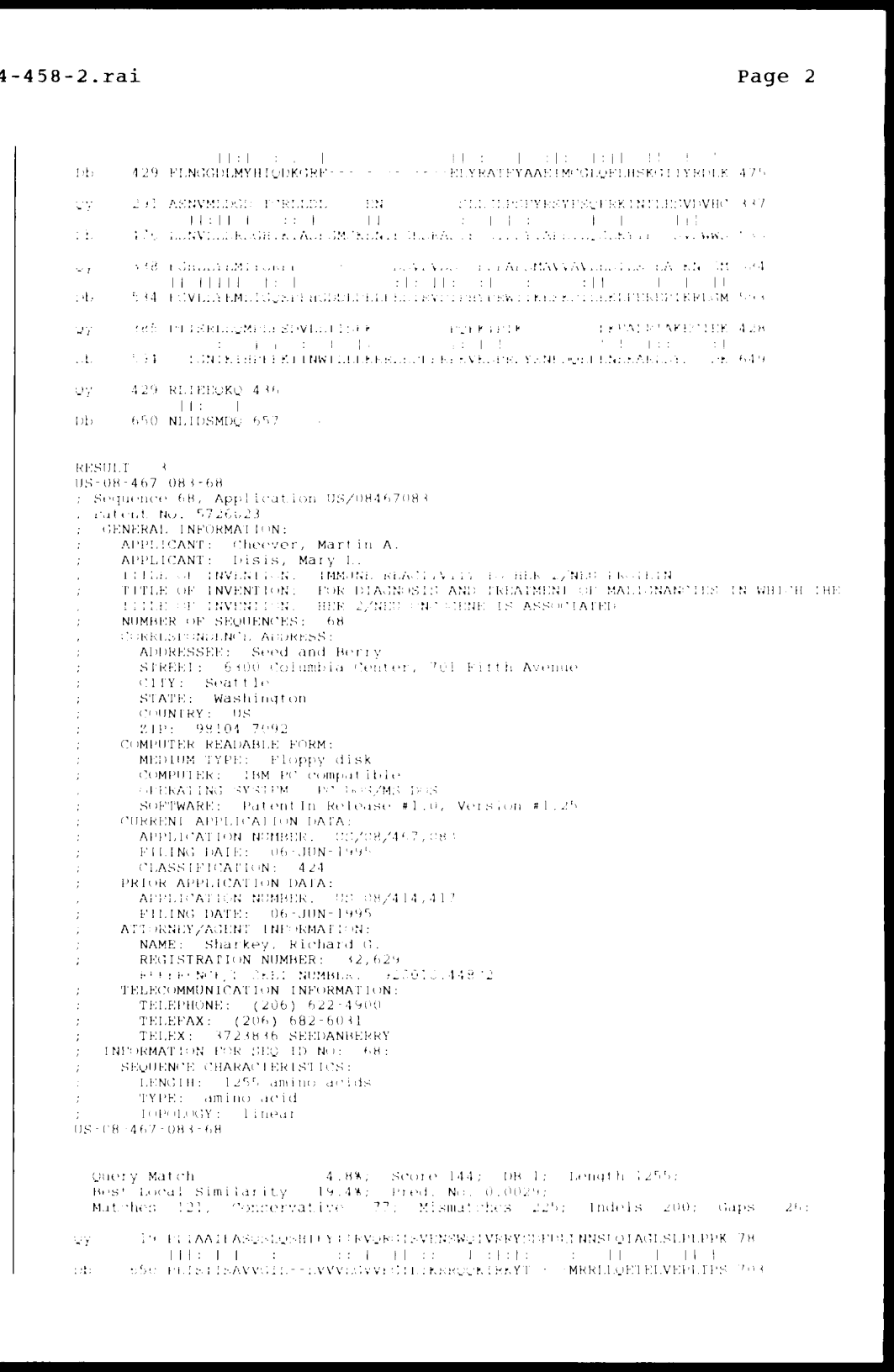
Result No.	Score	% Query Match	Length	DB	ID	Description
1	152.5	5.1	1297	2	US-08-290-731C-4	Sequence 4, Appli
2	145	4.8	676	4	US-09-313-530-2	Sequence 2, Appli
3	144	4.8	1255	1	US-08-467-083-68	Sequence 68, Appl
4	144	4.8	1255	1	US-08-414-417B-68	Sequence 68, Appl
5	144	4.8	1255	2	US-08-484-438-8	Sequence 8, Appli
6	144	4.8	1255	2	US-08-486-348A-68	Sequence 68, Appl
7	144	4.8	1255	2	US-08-625-101-2	Sequence 2, Appli
8	144	4.8	1255	2	US-08-468-545B-68	Sequence 68, Appl
9	144	4.8	1255	2	US-08-356-786-2	Sequence 2, Appli
10	144	4.8	1255	3	US-09-466-580B-68	Sequence 68, Appl
11	142	4.7	426	2	US-08-852-743-2	Sequence 2, Appli
12	142	4.7	426	2	US-09-2[illegible]-930-4	Sequence 4, Appli
13	142	4.7	426	3	US-09-340-993-4	Sequence 4, Appli
14	142	4.7	426	3	US-09-185-370-2	Sequence 2, Appli
15	142	4.7	426	4	US-09-152-406-4	Sequence 4, Appli
16	142	4.7	426	4	US-09-468-442-4	Sequence 4, Appli
17	141.5	4.7	430	4	US-09-152-406-3	Sequence 3, Appli
18	141	4.7	403	2	US-08-712-709-3	Sequence 3, Appli
19	141	4.7	403	3	US-09-111-414-3	Sequence 3, Appli
20	141	4.7	403	4	US-09-541-228-3	Sequence 3, Appli
21	138	4.6	652	1	US-08-318-831-8	Sequence 8, Appli
22	137.5	4.6	411	2	US-09-211-930-5	Sequence 5, Appli
23	137.5	4.6	411	3	US-09-340-993-5	Sequence 5, Appli
24	137.5	4.6	411	4	US-09-468-442-5	Sequence 5, Appli
25	136.5	4.5	580	1	US-08-414-417B-69	Sequence 69, Appl
26	136.5	4.5	580	2	US-08-486-348A-69	Sequence 69, Appl
27	136.5	4.5	580	2	US-08-468-545B-69	Sequence 69, Appl
28	136.5	4.5	580	3	[illegible]	Sequence 69, Appl
29	134	4.5	1315	3	US-08-899-[illegible]-3	Sequence 3, Appl
30	133	4.4	416	2	US-09-211-[illegible]	Sequence 3, Appl
31	133	4.4	416	3	[illegible]	Sequence 3, Appl
32	133	4.4	416	4	US-09-468-442-3	Sequence 3, Appl
33	133	4.4	694	3	[illegible]	Sequence 31, Appl
34	133	4.4	1248	2	[illegible]	Sequence 2, Appli
35	133	4.4	1248	4	[illegible]	Sequence 2, Appli
36	132.5	4.4	947	2	[illegible]	Sequence 2, Appli
37	132.5	4.4	947	2	[illegible]	Sequence 2, Appli
38	132.5	4.4	947	2	[illegible]	Sequence 2, Appli
39	132.5	4.4	947	4	[illegible]	Sequence 1, Appli
40	131	4.4	1255	2	[illegible]	Sequence 4, Appli
41	131	4.4	1255	3	[illegible]	Sequence 1, Appli
42	131	4.4	1255	4	[illegible]	Sequence 4, Appli
43	130	4.3	416	2	US-09-211-930-11	Sequence 11, Appl
44	130	4.3	416	3	US-09-340-993-11	Sequence 11, Appl
45	130	4.3	416	4	US-09-468-442-11	Sequence 11, Appl

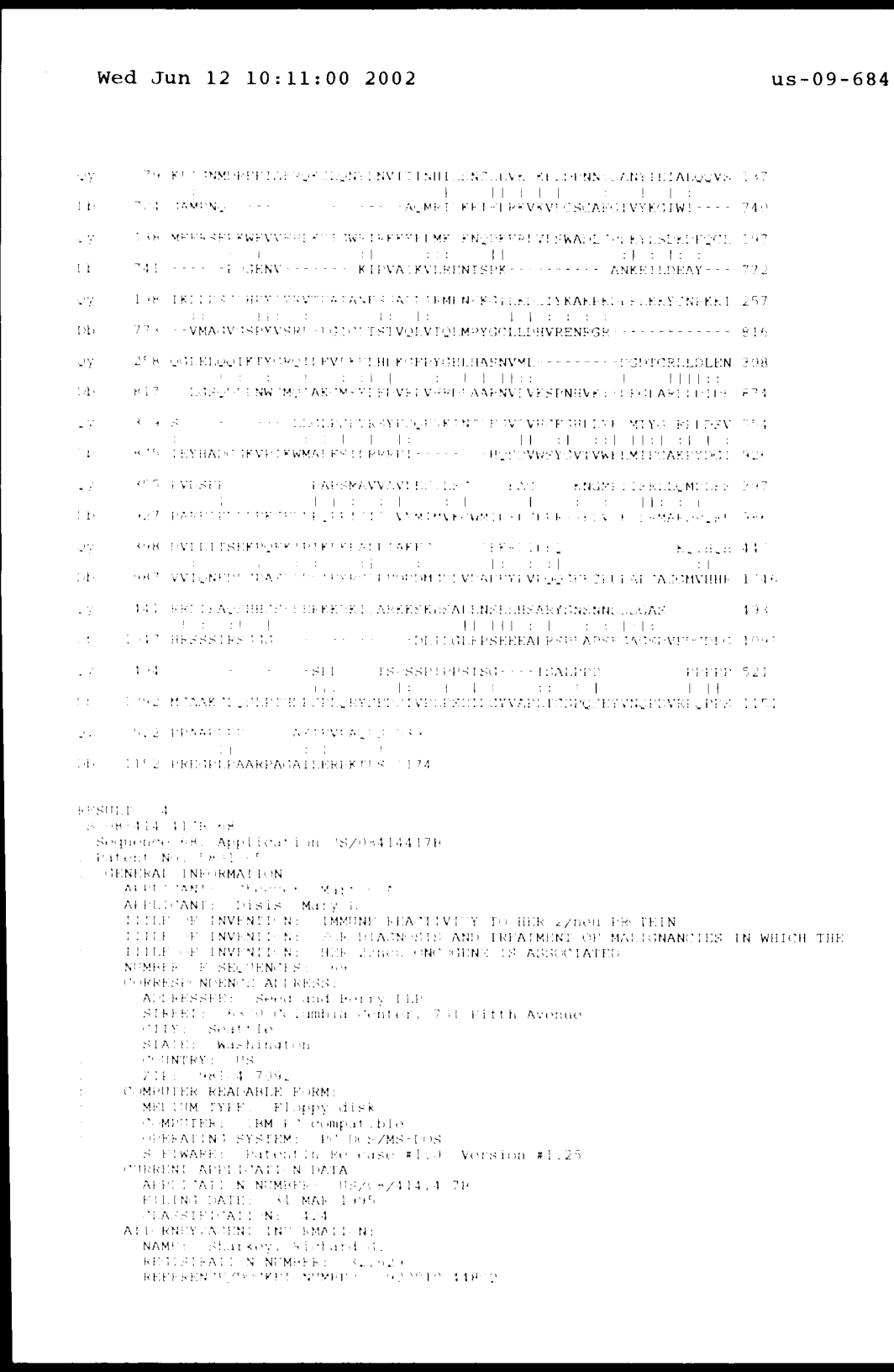
ALIGNMENTS

RESULT 1
US-08-290-731C-4
; Sequence 4, Application US/08290731C
; Patent No. 5843646
; GENERAL INFORMATION:
; APPLICANT: BOWTELL, David Douglas Lawrence
; TITLE OF INVENTION: DNA MOLECULES ENCODING MURINE
; TITLE OF INVENTION: [illegible]
; TITLE OF INVENTION: AND [illegible]PEPTIDES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/290,731C
; FILING DATE: 17 OCT 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU93/00068
; FILING DATE: 17-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PL0921/92
; FILING DATE: 17-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KIT, Gordon
; REGISTRATION NUMBER: 30,764
; REFERENCE/DOCKET NUMBER: Q-36066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1297 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-290-731C-4

Query Match 5.1%; Score 152.5; DB 2; Length 1297;

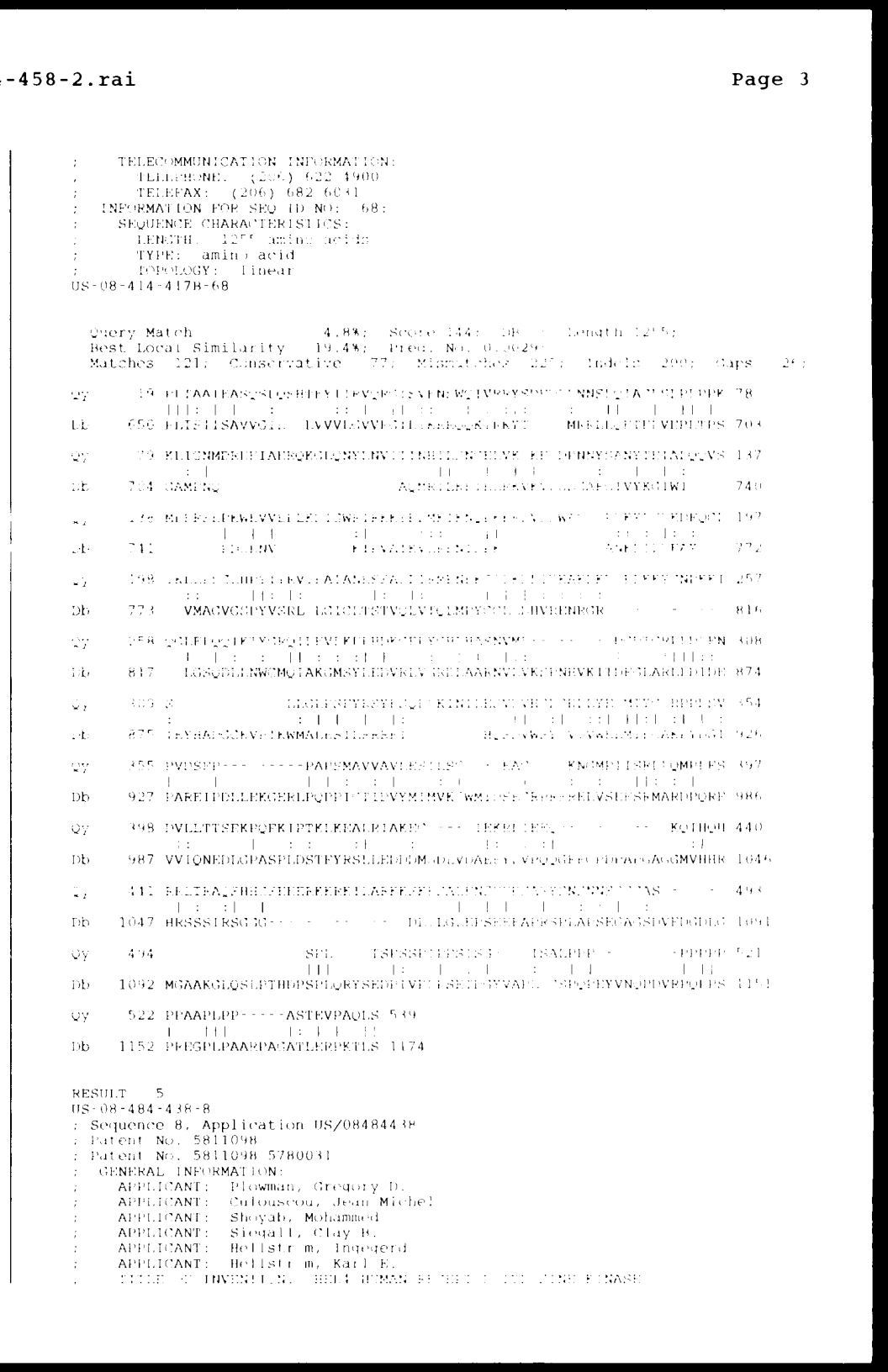






RESULT 4
US-08-414-417B-68
; Sequence 68, Application US/08414417B
; Patent No. 5811098
; GENERAL INFORMATION:
; APPLICANT: Stevens, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER 2/neu PROTEIN
; TITLE OF INVENTION: ASR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER 2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 63rd Floor Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA
; APPLICATION NUMBER: US/08/414,417B
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Starkey, Richard G.
; REGISTRATION NUMBER: 32,909
; REFERENCE/DOCKET NUMBER: 0290.410P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-414-417B-68

Query Match 4.8%; Score 144; DB 4; Length 1255;
Best Local Similarity 19.4%; Pred. No. 0.0029;
Matches 121; Conservative 77; Mismatches 327; Indels 209; Gaps 25;



RESULT 5
US-08-484-438-8
; Sequence 8, Application US/08484438
; Patent No. 5811098
; Patent No. 5811098 5780031
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory D.
; APPLICANT: Culouscou, Jean-Michel
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Sisgall, Clay B.
; APPLICANT: Hollister m, Ingegerd
; APPLICANT: Hollister m, Karl E.
; TITLE OF INVENTION: BETA HEREGULIN RECEPTOR

```
;       NUMBER OF SEQUENCES: 42
;       CORRESPONDENCE ADDRESS:
;         ADDRESSEE: Pennie & Edmonds
;         STREET: 1155 Avenue of the Americas
;         CITY: New York
;         STATE: New York
;         COUNTRY: U.S.A.
;         ZIP: 10036-2711
;       COMPUTER READABLE FORM:
;         MEDIUM TYPE: Floppy disk
;         COMPUTER: IBM PC compatible
;         OPERATING SYSTEM: PC-DOS/MS-DOS
;         SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;         APPLICATION NUMBER: US/08/484,168
;         FILING DATE: 07-JUN-1995
;         CLASSIFICATION: 530
;       PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: 08/323,442
;         FILING DATE: 14-OCT-1994
;         APPLICATION NUMBER: US 08/150,704
;         FILING DATE: 10-NOV-1993
;         CLASSIFICATION: 530
;       PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: US 07/981,165
;         FILING DATE: 24-NOV-1992
;         CLASSIFICATION: 530
;       ATTORNEY/AGENT INFORMATION:
;         NAME: Misrock, S. Leslie
;         REGISTRATION NUMBER: 18,872
;         REFERENCE/DOCKET NUMBER: 5621-230
;       TELECOMMUNICATION INFORMATION:
;         TELEPHONE: (212) 790-9090
;         TELEFAX: (212) 869-8864/9741
;         TELEX: 66141 PENNIE
;     INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH: 1255 amino acids
;         TYPE: amino acid
;         STRANDEDNESS: unknown
;         TOPOLOGY: unknown
;       MOLECULE TYPE: protein
US-08-484-168-8

  Query Match             4.8%;  Score 144;  DB 2;  Length 1255;
  Best Local Similarity   19.1%;  Pred. No. 0.0029;
  Matches 120;  Conservative  80;  Mismatches 230;  Indels 198;  Gaps  26;

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Qy      79 KLIGNMDREFIAERQKGLQNYLNVITTNHILSNCELVKKFLDPNNYSANYTEIALQQVS 137
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Qy     138 MFFRSEPKWEVVEPLKEIGWRIPKKYLLMKIKNQFKERLVLSWADLQPEKYLQQKDPQCL 197
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Qy     355 PVDSFP-----------PAPSMAVVAVLESILSC----EAC--  KNGMPFISRLLQMPLPS 397
Db     927 PAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRF 986

Qy     398 DVLLIISEKPQ[illegible]KEALFIAKEC   [illegible]KRLIEEQ--      -   KQIHQH 440
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Qy     441 [illegible]GNNSGSAS      493
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Qy     494                   SPL    TSPSSPTPPSTSG-  ISALPPP   -    PPPPP 521
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Qy     522 PPAAPLPPASIEVPAQLSSQAVNGMSRG 549
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RESULT 6
US-08-486-348A-68
; Sequence 68, Application US/08486348A
; Patent No. 5846538
;  GENERAL INFORMATION:
;    APPLICANT: Cheever, Martin A.
;    APPLICANT: Disis, Mary L.
;    TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
;    TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
;    TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
;    NUMBER OF SEQUENCES: 69
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: Seed and Berry LLP
;      STREET: 6300 Columbia Center, 701 Fifth Avenue
;      CITY: Seattle
;      STATE: Washington
;      COUNTRY: US
;      ZIP: 98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/486,348A
;      FILING DATE: 07-JUN-1995
;      CLASSIFICATION: 424
;    ATTORNEY/AGENT INFORMATION:
;      NAME: Sharkey, Richard G.
;      REGISTRATION NUMBER: 32,629
;      REFERENCE/DOCKET NUMBER: 920010.448C6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (206) 622-4900
;      TELEFAX: (206) 682-6031
;  INFORMATION FOR SEQ ID NO: 68:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 1255 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
US-08-486-348A-68

  Query Match             4.8%;  Score 144;  DB 2;  Length 1255;
  Best Local Similarity   19.4%;  Pred. No. 0.0029;
  Matches 121;  Conservative  77;  Mismatches 227;  Indels 200;  Gaps  26;

Qy      19 PLIAAIEASQSLQSHTEYIIRVQRGISVENSWQIVRRYSDFDLLNNSLQIAGLSLPLPPK 78
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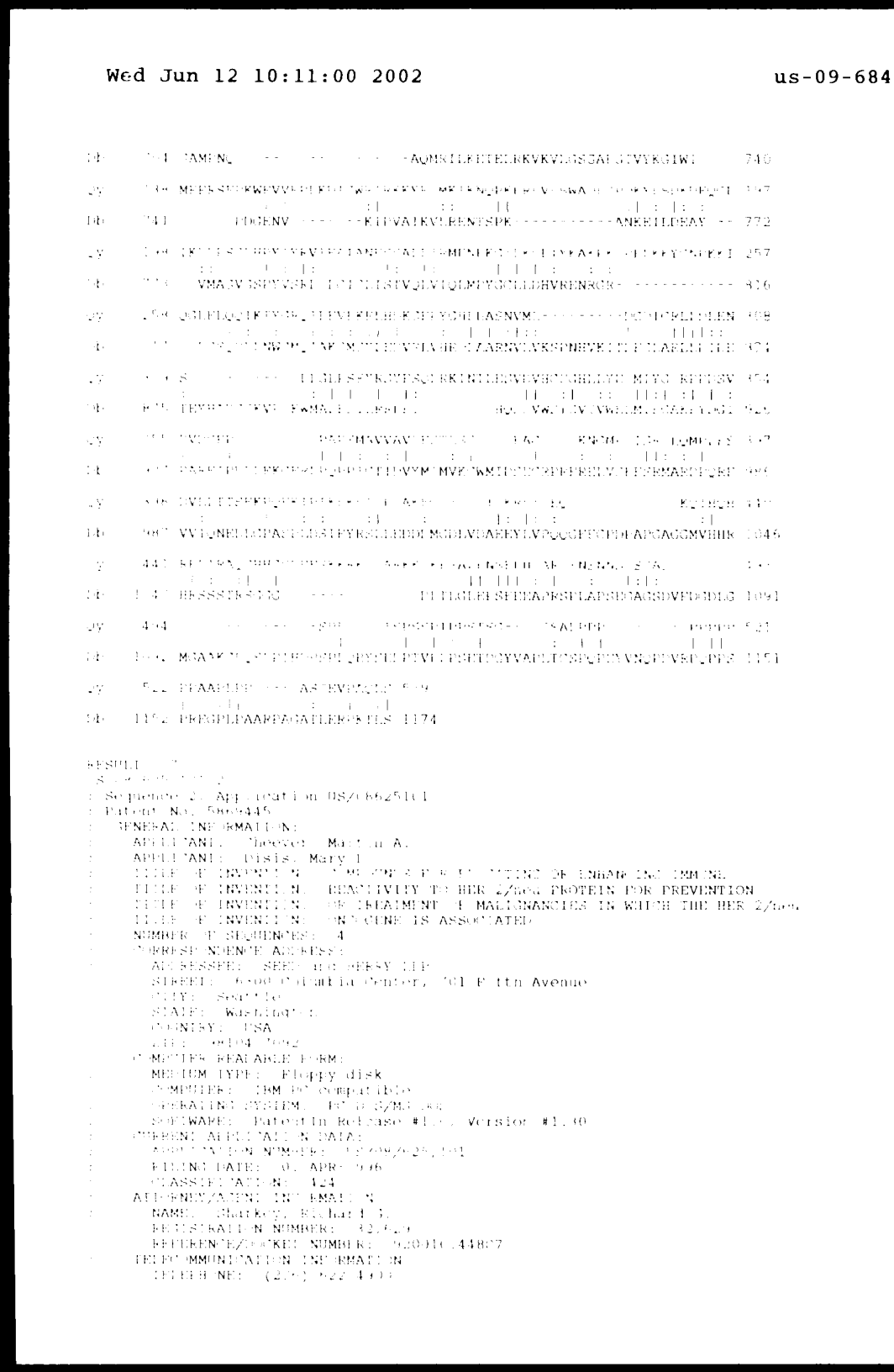

; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-625-101-2

Query Match 4.8%; Score 144; DB 2; Length 1255;
Best Local Similarity 19.4%; Pred. No. 2.2e-23;
Matches 121; Conservative 77; Mismatches 422; Indels 200; Gaps 24;

RESULT 8
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; Sequence 68, Application US/08468545A
; Patent No. 5876712
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY T HER 2/neu PROTEIN
; TITLE OF INVENTION: FOR TREATMENT AN TREATMENT T MALIGNANCIES IN WITCH THE
; TITLE OF INVENTION: HER 2/neu GEN IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry II
; STREET: 6300 Columbia Center, 701 Fifth Avenue

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;       CITY:  Seattle
;       STATE:  Washington
;       COUNTRY:  US
;       ZIP:  98104-7092
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/468,545B
;       FILING DATE:  06-JUN-1995
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Sharkey, Richard G.
;       REGISTRATION NUMBER:  32,629
;       REFERENCE/DOCKET NUMBER:  920010.448C5
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206) 622-4900
;       TELEFAX:  (206) 682-6031
;   INFORMATION FOR SEQ ID NO:  68:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1255 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
US-08-468-545B-68

  Query Match             4.8%;  Score 144;  DB 2;  Length 1255;
  Best Local Similarity   19.4%;  Pred. No. 0.0029;
  Matches  121;  Conservative   77;  Mismatches  225;  Indels  200;  Gaps   26;

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Qy        138 MFFPSEPKWEVVEPLKDICWRIRKKYEIMKIKNQPKERLVLSWADLGPDKYLSQKDFQCL 197
                 |   |   |          :|        :::      ||                  :  :  : | :  :
Db        741       PDGENV         KIPVAIKVLRENISPK                   ANKEILDEAY    772

Qy        198 IKLLPSCLHPYIYRVIFATANESSALLIRMFNEKGILKPLIYKAKPKDPFLKKYCNPKKI 257
                       ||:   :           |:   |:         |  |  |   :  :  :  :
Db        773   VMAGVGSPYVSRL-LGICLISTVQLVIQLMPYGCLLDHVRENRGR--      ----  816

Qy        258 QGLELQQIKIYGRQILEVLKFLHDKGFPYGHLHASNVML --   --- DGDTCRLLDLEN 308
                          :  :  :  :  :| |      :   |  |  :|::                |        ||||::
Db        817   LGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLVKSPNHVKITDFGLARLLDIDE 874

Qy        309                  IIGLPSFYRSYFSQFRKINTLESVDVHCFGHLLYE MIYG RPPDSV 354
                                :  |   |    |   |:                  :|    :|    ::|  ||:|  :|  |  :
Db        875 TEYHADGGKVPIKWMALESILRRRFT           HQSDVWSYGVTVWELMTFGAKPYDGI 926

Qy        355 PVDGEF               PAPSMAVVAVLESILSC        EAC --  KNGMPIISRLLQMPLFS 397
                 :        |                 |  |  :  :  |     :  |           |        :     :      | | :  :  |
Db        927 IAREIPDLLEKGERLPQPPICTIDVYMIMVKCWMIDSECRPRFRELVSEFSRMARDPQRF 986

Qy        398 FVILTISEKPQEKIPTKLKEALRIAKE    -     IEKRLIEEQ------  ---  KQIHQE 449
                   :         :  :        :|          :               |:  |:  :|                :|
Db        987 VVIQNEDLGPASPLDSTFYRSLLEDDDMGDLVDAEEYLVPQQGFFCPDPAPGAGGMVHHR 1046

Qy        441 KKLIRAQSHHGSEEKKKRKTLAKKKSKRSALENSEEHSAKYSNSNNSGSGAS-------- 493
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Db       1047 HRSSSTRSGGG          -       DLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGDLG 1091

Qy        494                           SPL       ISPSSPTPPSISG-      ISALPPP-     -      PPPPP 521
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Db       1092 MGAAKGLQSLPTHDPSPLQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPS 1151

Qy        522 PPAAPLPP        ASIEVPAQLS 539
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Db       1152 PREGPLPAARPAGATLERPKTLS 1174

RESULT 9
US-08-356-786-2
; Sequence 2, Application US/08356786
; Patent No. 5877305
;  GENERAL INFORMATION:
;    APPLICANT:  Huston, James S.
;    APPLICANT:  Oppermann, Hermann
;    APPLICANT:  Houston, L. L.
;    APPLICANT:  Ring, David B.
;    TITLE OF INVENTION:  Biosynthetic Binding Protein for Cancer
;    TITLE OF INVENTION:  Marker
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
;      STREET:  Exchange Place, 53 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/356,786
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/831,967
;      FILING DATE:  06-FEB-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pitcher, Edmund R.
;      REGISTRATION NUMBER:  27,829
;      REFERENCE/DOCKET NUMBER:  CRP-053
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1255 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-356-786-2

  Query Match             4.8%;  Score 144;  DB 2;  Length 1255;
  Best Local Similarity   19.4%;  Pred. No. 0.0029;
  Matches  121;  Conservative   77;  Mismatches  225;  Indels  200;  Gaps   26;

Qy         19 PLTAAIEASQSLQSHIEYIIRVQRGISVENSWQIVRRYSDFDLLNNSLQIAGLSLPLPPK 78
                 |||: | |    :          :: |  ||  :    :  :|:|:      :    ||    |  |||
Db        650 PLTSIISAVVGIL--LVVVLGVVFGILIKRRQQKIRKYI--MRRLLQETELVEPLTPS 703

Qy         79 KLIGNMDREFIAERQKGLQNYLNVIINHILSNCELVK-KFLDPNNYSANYIEIALQQVS 137
                :  |                               ||    ||  |  |  |      :     |    | :
Db        704 GAMPNQ                       AQMRILKETELRKVKVLGSGAFGTVYKGIWI---- 740

Qy        138 MFFPSEPKWEVVEPLKDICWRIRKKYEIMKIKNQPKERLVLSWADLGPDKYLSQKDFQCL 197
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Db        741 ------PDGENV--------KIPVAIKVLRENISPK   -   ---ANKEILDEAY--- 772

Qy        198 IKLLPSCLHPYIYRVIFATANESSALLIRMFNEKGILKPLIYKAKPKDPFLKKYCNPKKI 257
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Db        773 --VMAGVGSPYVSRL-LGICLISTVQLVIQLMPYGCLLDHVRENRGR--          816

Qy        258 QGLELQQIKIYGRQILEVLKFLHDKGFPYGHLHASNVML            DGDTCRLLDLEN 308
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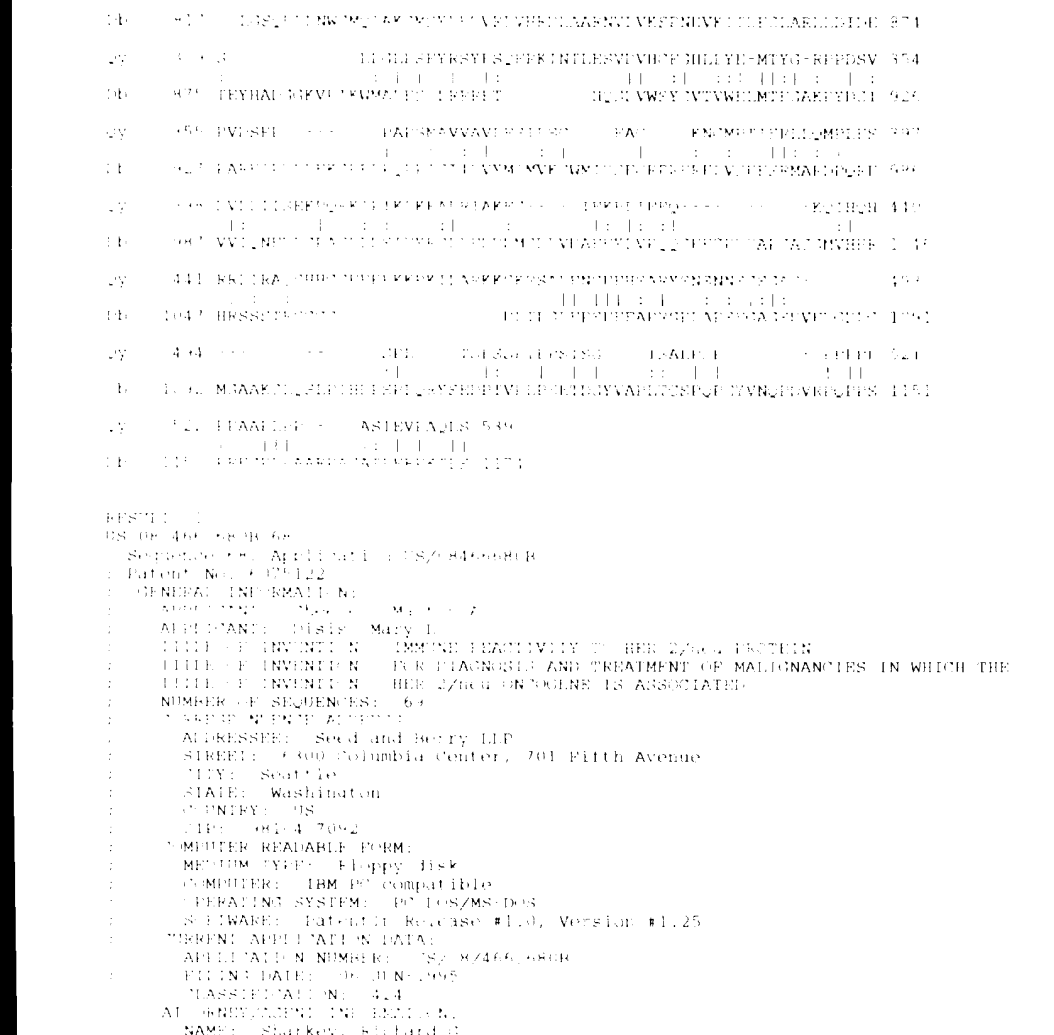
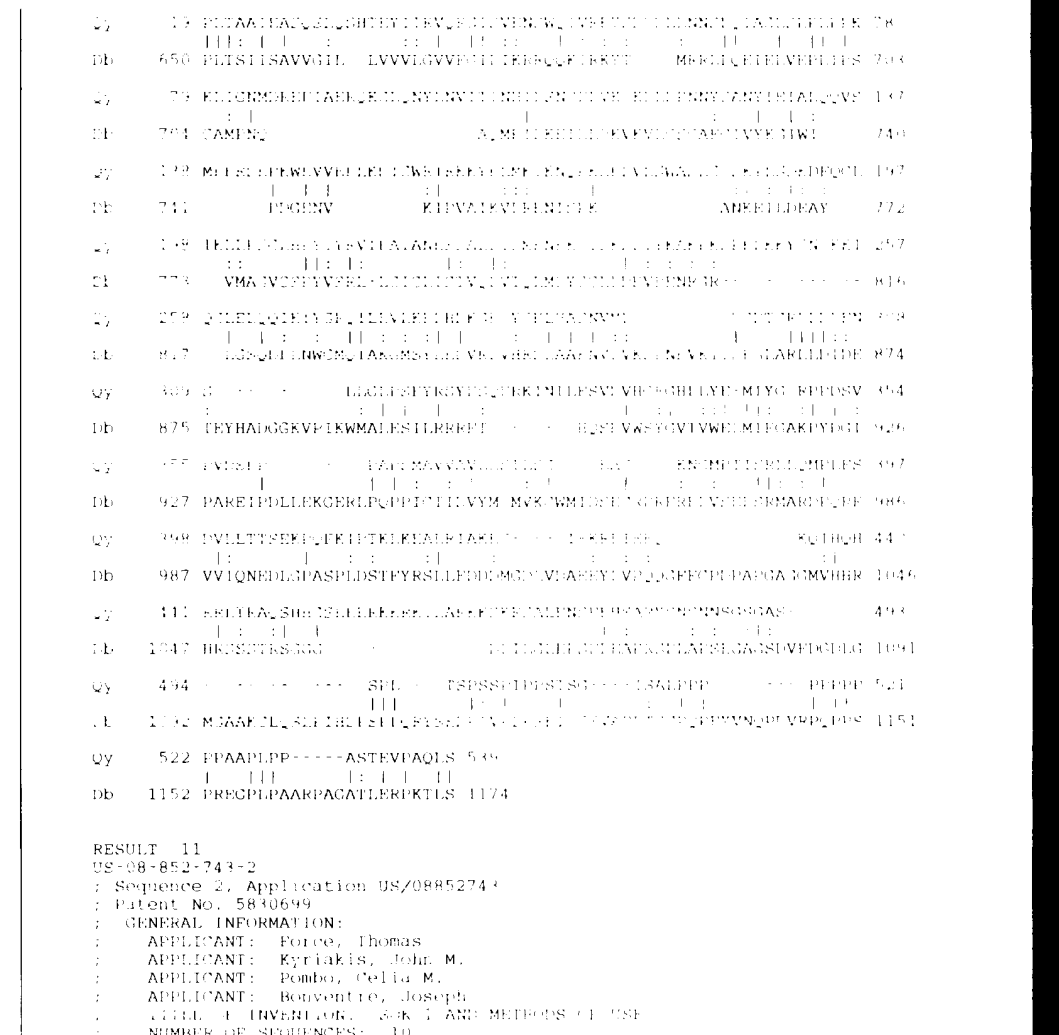
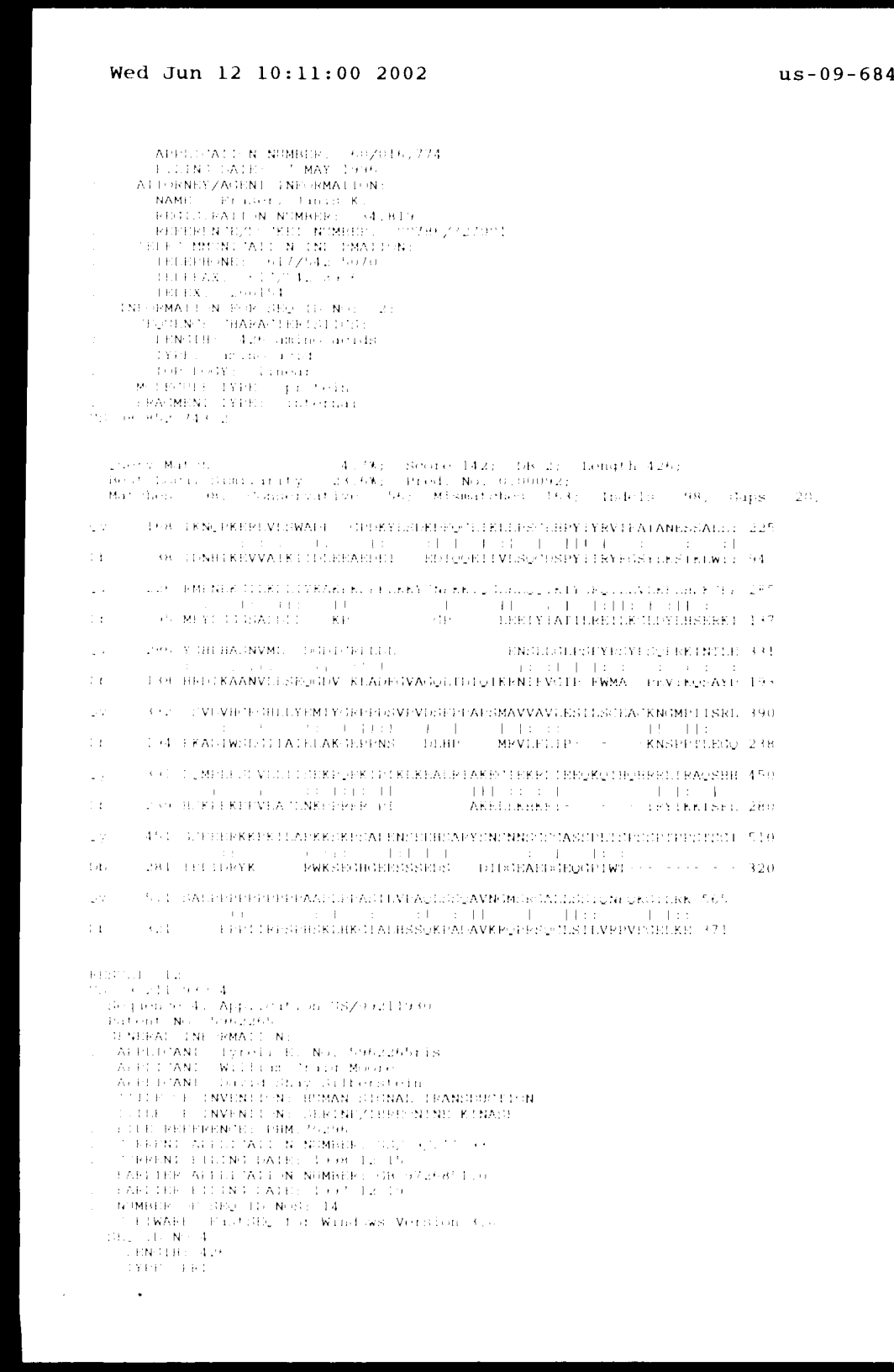


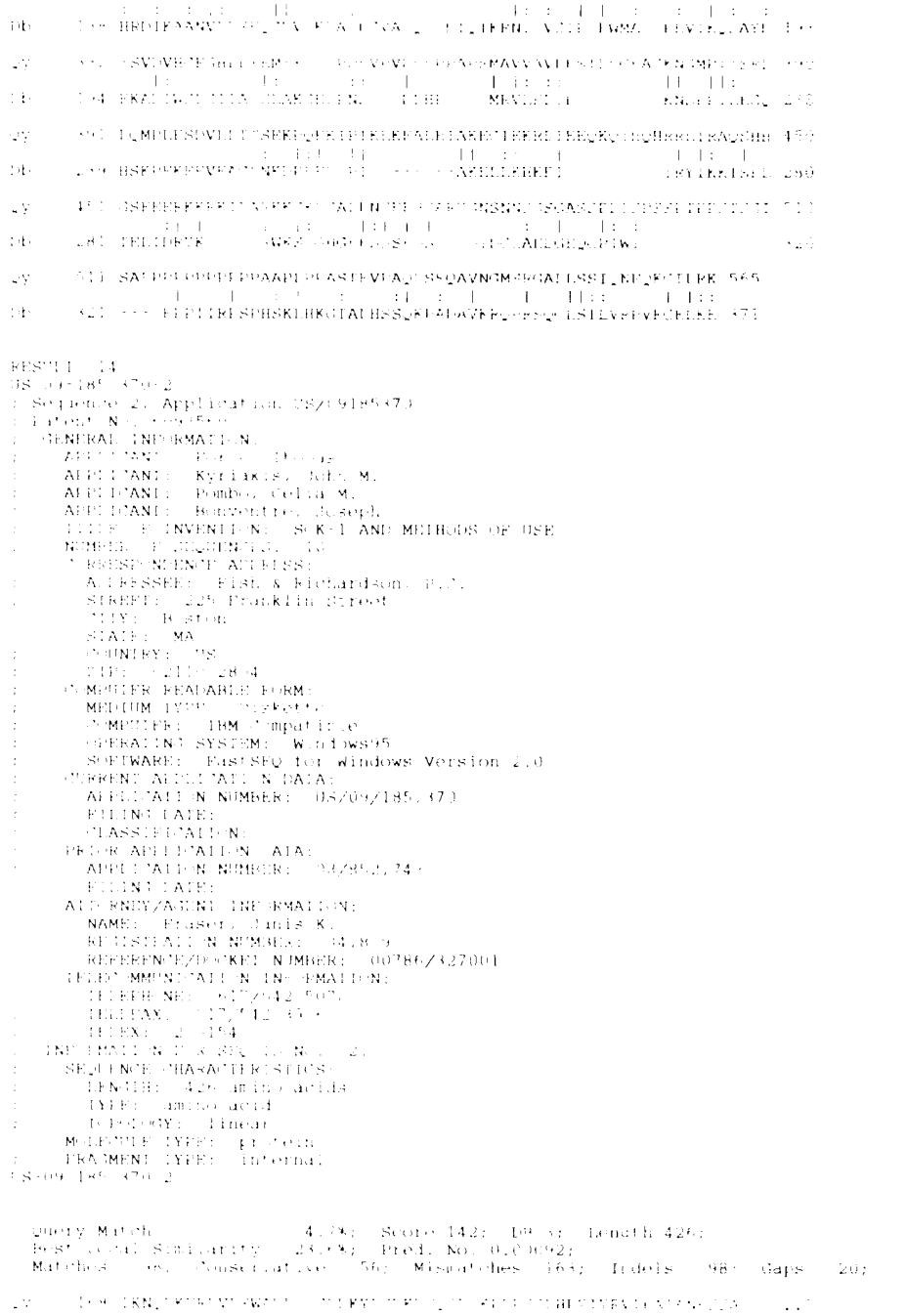
RESULT 1
US-09-684-458-2
; Sequence 2, Application US/09684458
; Patent No. 6407122
; GENERAL INFORMATION:
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/466,080B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Starkey, Richard D.
; REGISTRATION NUMBER: 31,462
; REFERENCE/DOCKET NUMBER: 020010.4404
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

Query Match 4.8%; Score 114; DB 4; Length 1255;
Best Local Similarity 16.4%; Pred. No. 0.0029;
Matches 127; Conservative 77; Mismatches 225; Indels 200; Gaps 25;



RESULT 11
US-08-852-743-2
; Sequence 2, Application US/08852743
; Patent No. 5830699
; GENERAL INFORMATION:
; APPLICANT: Force, Thomas
; APPLICANT: Kyriakis, John M.
; APPLICANT: Pombo, Celia M.
; APPLICANT: Bonventre, Joseph
; TITLE OF INVENTION: JUK I AND METHODS OF USE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/852,743
; FILING DATE: 7-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:





RESULT 14
US-09-185-870-2
; Sequence 2, Application US/09185870
; Patent No. 6265560
; GENERAL INFORMATION:
; APPLICANT: Kyriakis, John M.
; APPLICANT: Pombo, Celia M.
; APPLICANT: Bonventre, Joseph
; TITLE OF INVENTION: SOK-1 AND METHODS OF USE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/185,870
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/895,274
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00780/327001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-185-870-2

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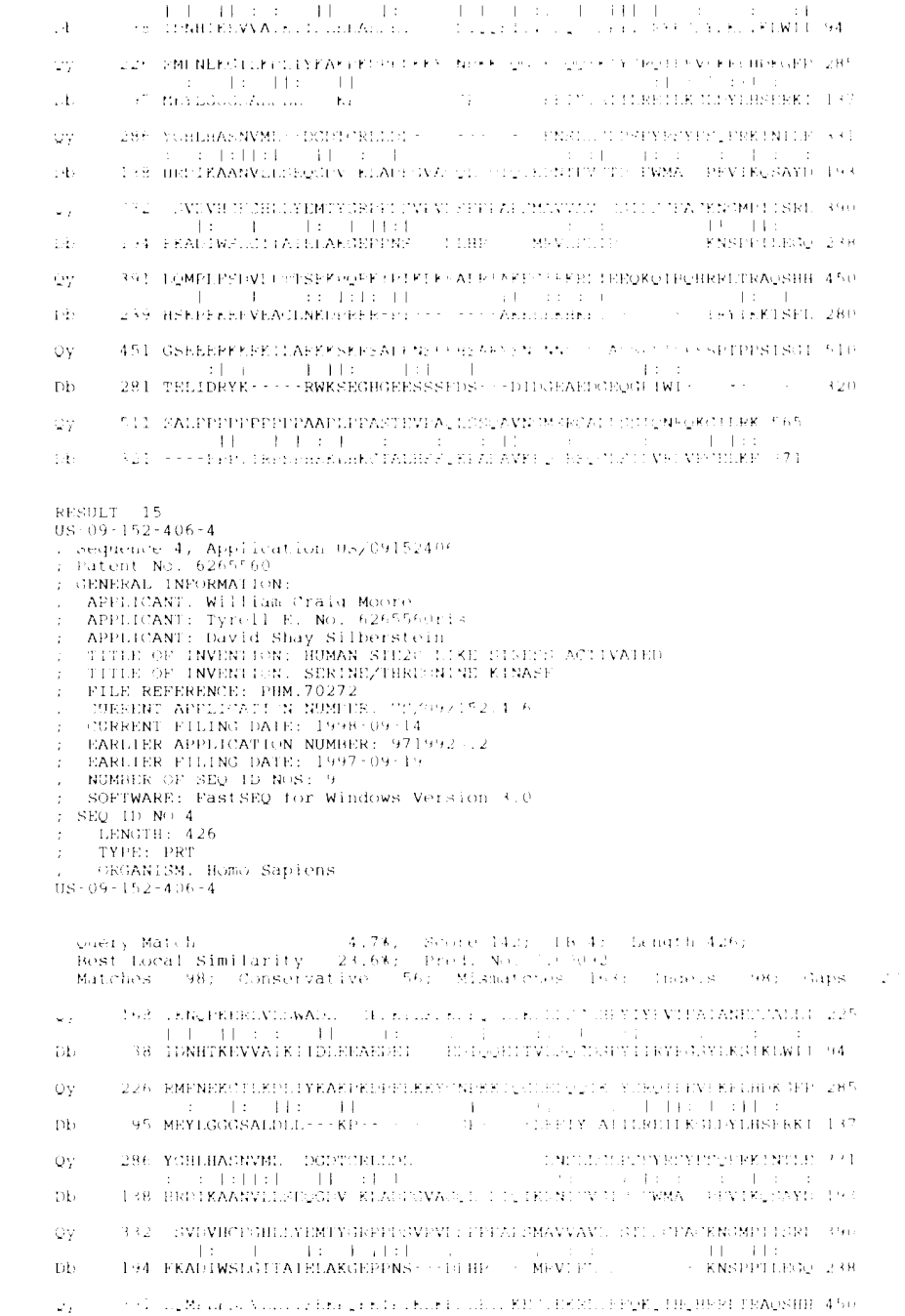
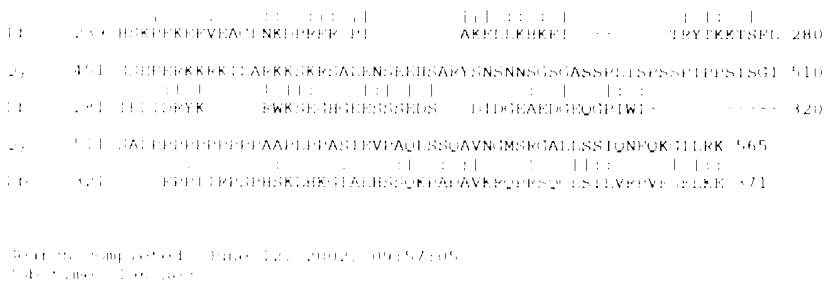
Best Local Similarity 23.6%; Pred. No. 0.0092;
Matches 98; Conservative 56; Mismatches 163; Indels 98; Gaps 20;



RESULT 15
US-09-152-406-4
; Sequence 4, Application Us/09152406
; Patent No. 6265560
; GENERAL INFORMATION:
; APPLICANT: William Craig Moore
; APPLICANT: Tyrell E. No. 626560rls
; APPLICANT: David Shay Silberstein
; TITLE OF INVENTION: HUMAN SIL2 LIKE SIGE5 ACTIVATED
; TITLE OF INVENTION: SERINE/THRESHNINE KINASE
; FILE REFERENCE: PHM.70272
; PRESENT APPLICATION NUMBER: US/09/152,406
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: 971992.2
; EARLIER FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-152-406-4

Query Match 4.7%; Score 142; DB 4; Length 426;
Best Local Similarity 24.6%; Pred. No. 0.0092;
Matches 98; Conservative 56; Mismatches 163; Indels 98; Gaps 20;



GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

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(without alignments)
[illegible].059 Million cell updates/sec

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Perfect score: [illegible]
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 17[illegible]4929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_1[illegible]:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	[illegible]	97.3	649	4	Q9NXB8	Q9nxb8 homo sapien
2	[illegible]	[illegible]	582	11	Q91WB6	Q91wb6 mus musculu
3	2620.5	87.3	515	4	Q96R07	Q96r07 homo sapien
4	[illegible]	78.3	450	4	Q96CA3	Q96ca3 homo sapien
5	[illegible]	2[illegible].3	450	5	Q95RK3	Q95rk3 drosophila
6	[illegible]74	2[illegible].1	56[illegible]	5	Q9V344	Q9v344 drosophila
7	39[illegible].5	13.1	515	5	O61564	O61564 drosophila
8	39[illegible].5	13.1	515	5	Q9VLZ4	Q9vlz4 drosophila
9	35[illegible]	11.9	280	5	Q95SL3	Q95sl3 drosophila
10	211.5	7.0	496	4	Q96BR1	Q96br1 homo sapien
11	2[illegible]4.5	[illegible].8	49[illegible]	11	Q9ERE3	Q9ere3 mus musculu
12	18[illegible]	6.1	1851	5	Q18657	Q18657 caenorhabdi
13	17[illegible]	5.9	1112	4	Q96PY5	Q96py5 homo sapien
14	172	5.7	1231	4	Q96DT8	Q96dt8 homo sapien
15	172	5.7	124[illegible]	4	Q96J92	Q96j92 homo sapien
16	172	5.7	2126	11	Q9JIH7	Q9jih7 rattus norv
17	171.5	5.7	670	4	Q9P[illegible]S9	Q9p[illegible]s9 homo sapien
18	171.5	5.7	1228	5	O17566	O17566 caenorhabd
19	171.5	5.7	2382	4	Q9H4A[illegible]	Q9h4a[illegible] homo sapien
20	166	5.5	513	13	Q9DEQ2	Q9deq2 gallus gal
21	164.5	5.5	1043	5	Q9V[illegible]	Q9v[illegible] drosophila
22	163	5.4	1504	4	Q9HES6	Q9hes6 homo sapien
23	163	5.4	1528	4	Q9Y[illegible]1	Q9y[illegible]1 homo sapien
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26	161.5	5.4	1062	5	Q9[illegible]	Q9[illegible] caenorhabdi
27	159	5.3	779	4	Q9H[illegible]4	Q9h[illegible]4 homo sapien
28	158.5	5.3	550	13	O93263	O93263 gallus gal
29	158.5	5.3	1032	16	Q9I758	Q9i758 pseudomonas
30	158	5.3	901	10	Q9[illegible]48R7	Q9[illegible]48r7 oryza sativ
31	158	5.3	1206	11	[illegible]88[illegible]5	[illegible]8815 rattus norv
32	158	5.3	1231	11	[illegible]	[illegible] cavia porce
33	157.5	5.2	1189	5	Q9Y111	Q9y111 drosophila
34	157.5	5.2	1189	5	Q9W378	Q9w378 drosophila
35	156	5.2	429	4	Q9HKG5	Q9hkg5 homo sapien
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37	155.5	5.2	1202	11	Q9WU41	Q9wu41 mus musculu
38	155.5	5.2	1233	11	O54988	O54988 mus musculu
39	155.5	5.2	1450	4	Q9BYP7	Q9byp7 homo sapien
40	154.5	5.1	907	10	Q9C946	Q9c946 arabidopsis
41	153.5	5.1	643	2	Q9S478	Q9s478 myxococcus
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43	153.5	5.1	1621	5	O01900	O01900 caenorhabdi
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45	152.5	5.1	1032	2	Q9ZIB2	Q9zib2 pseudomonas

ALIGNMENTS

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DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawakami T., Noguchi S., Itoh I., Shiga[illegible] K., Senta [illegible]., Matsumura K.,
RA Nakajima Y., Mizuno T., Morinaga M., [illegible]ta T., Sasaki Y., Obayashi M.,
RA Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AK000342; BAA91097.1; -.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR001683; PX.
DR InterPro; IPR003124; WH2.
DR Pfam; PF0228[illegible]; WH2; 1.
DR SMART; SM00312; PX; 1.
DR SMART; SM00246; WH2; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP binding; Transferase.
FT NON_TER 649 649
SQ SEQUENCE 649 AA; 73060 MW; [illegible] CRC64;

Query Match 97.3%; Score 2919.5; DB 4; Length 649;
Best Local Similarity 96.3%; Pred. No. [illegible];
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DE   SIMILAR TO HYPOTHETICAL PROTEIN FLJ20335.
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID [illegible];
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SALIVARY GLAND;
RA   Strausberg R.;
RL   Submitted ([illegible]) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; [illegible]; AAH[illegible].1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   582 AA;   65201 MW;   ED55496B61F2E9AA CRC64;

  Query Match [illegible]; Score [illegible]; DB 11; Length 582;
  Best Local Similarity [illegible]; Pred. No. [illegible];
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Db          1 MA[illegible]MEKPPA[illegible]KV[illegible]DIVPLIAAVEASQSLQSHIEY[illegible]RVQRGISAENSWQIVRRYSDFD 60

Qy         61 [illegible]LNN[illegible]NM[illegible]FIAERQ[illegible]NYLNV[illegible]VKKFLD 120
Db         61 [illegible]NNS[illegible]KKL[illegible]NMERFIAERQR[illegible]NYLNVIMANHVL[illegible]LLKKFLD 120

Qy        121 [illegible]NNY[illegible]ANY[illegible]VSMF[illegible]KWEVVEPLK[illegible]WKIRKKYFLMKIENQPKERLVLSW 180
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Db        121 [illegible]VLSW 180

Qy        181 A[illegible]IYK 240
Db        181 A[illegible] 240

Qy        241 AK[illegible]NVM[illegible] 300
Db        241 AK[illegible]AANVM[illegible] 300

Qy        301 CRLLDLENSLLGLPSFYRSYFSQFRKINILESVDVHCFGHLLYEMIYGRPFDSVPVPSFP 360
Db        301 [illegible] 360

Qy        361 [illegible]MAVVAV[illegible]ELALR 420
Db        361 FASSLAVVAVLESTLS[illegible]KNGMPIVSPLLQMPLPSDVLLIISEKPQEKIPIKLKEALR 420

Qy        421 IAKE[illegible]SA 480
Db        421 IAK[illegible]AVENSEEQPV 480

Qy        481 RYGNGNNG[illegible]GAGSSPLISPSSPIPPSTSGTSAL      PPPPPPPPAAPLPPASTEVL 535
Db        481 K[illegible]PAISPTSAIEIP 540

Qy        536 A[illegible]AVN[illegible]AL[illegible]AK[illegible]HSAPKIG 577
Db        541 A[illegible]VN[illegible]AL[illegible] 582
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RESULT 3
Q96R07
ID   Q96R07   PRELIMINARY;   PRT;   515 AA.
AC   Q96R07;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PX DOMAIN CONTAINING PROTEIN KINASE.
GN   PXK.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID 9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hong W.;
RT   "PXK, a novel PX domain-containing protein kinase.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF399753; AAK94455.1; -.
KW   Kinase.
SQ   SEQUENCE   515 AA;   58660 MW;   FA63A4F5127C0D44 CRC64;

  Query Match 87.3%; Score 2620.5; DB 4; Length 515;
  Best Local Similarity 99.6%; Pred. No. 2.5e-178;
  Matches 507; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy          1 MAFMEKPPAGKVLLDDIVPLIAAIEASQSLQSHIEYIIRVQRGISVENSWQIVKRYSDFD 60
Db          1 MAFMEKPPAGKVLLDDIVPLIAAIEASQSLQSHIEYIIRVQRGISVENSWQIVKRYSDFD 60

Qy         61 LLNNSLQIANISLPLPPKKLIGNMDREFIAERQKGLQNYLNVITTNHILSNCELVKKFLD 120
Db         61 LLNNSLQIANISLPLPPKKLIGNMDREFIAERQKGLQNYLNVITTNHILSNCELVKKFLD 120

Qy        121 PNNYSANYTEIALQQVSMFFRSEPKWEVVEPLKDIGWRIRKKYFLMKIENQPKERLVLSW 180
Db        121 PNNYSANYTEIALQQVSMFFRSEPKWEVVEPLKDIGWRIRKKYFLMKIENQPKERLVLSW 180

Qy        181 ADLGPDKYLSDKDFQCLIKLLPSCLHPYIYRVTFATANESSALLIRMFNEKGTLKDLIYK 240
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Db    [illegible] 240

Qy    241 AKPK[illegible]KKY[illegible]NPKK[illegible]PVLKPLHDKGPFY[illegible]HLHASNVML[illegible] 300
Db    241 AKPK[illegible]KKY[illegible]NPKK[illegible]LVLKPLHDKGPFY[illegible]HLHASNVMLDGDT 300

Qy    301 [illegible]KINTLESVDVHCFGHLLYEMT[illegible]GRPFDSVPVDSFP 360
Db    301 CRLLDLENSLLGLPSFYRSYFSQFPKINTLESVDVHCFGHLLYIMIYGRPFDSVPVDSFP 360

Qy    361 PAPSMAVVAVLESILSCEACKNGMPTTSELQMPLESDVLLTTSEKEQFKIPTKLKEALR 420
Db    361 PAPSMAVVAVLESILSCEACKNGMPTTSELQMPLESDVLLTTSEKEQFKIPTKLKEALR 420

Qy    421 IAK[illegible]AKKESE[illegible]ALENSLGHSA 480
Db    421 IAK[illegible]AKKESE[illegible]ALENSEGHSA 480

Qy    481 RYSNGNNS[illegible]GSASSPLISLSSPTTPSTS 508
Db    481 RYSNGNNSAGSGASSPLISLSSPTTPSTS 509


RESULT 4
Q96[illegible]A8
ID   Q96[illegible]A8      PRELIMINARY;      PRT;   450 AA.
AC   Q96[illegible]A8;
DT   [illegible] (TrEMBLrel. 19, Created)
DT   [illegible] (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL [illegible] KDA PROTEIN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID [illegible];
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PRIMARY B-CELLS FROM [illegible];
RA   Strausberg R.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC014479; AAH14479.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   450 AA;  518[illegible] MW;  [illegible]B70B407EF CRC64;

  Query Match             78.3%;  Score 2350;  DB 4;  Length 450;
  Best Local Similarity   100.0%;  Pred. No. [illegible];
  Matches  450;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MAEMPKPLA[illegible]KVL[illegible]IVPLIAAIEASQSLQSHIEYIIRVQRGLSVENSWQIVRRYSDFD 60
Db      1 MAEMEKPFAGKVL[illegible]IVPLIAAIEASQSLQSHIEYIIRVQRGLSVENSWQIVRRYSDFD 60

Qy     61 [illegible]LNNSL[illegible]IA[illegible]PKKL[illegible]NMD[illegible]IAER[illegible]LQNY[illegible]NVIIENH[illegible]ELVKKFLD 120
Db     61 [illegible]LNNSL[illegible]IA[illegible]PKKL[illegible]NMD[illegible]IAER[illegible]LQNY[illegible]NVIIENH[illegible]ELVKKFLD 120

Qy    121 PNNY[illegible]ANYTE[illegible]AL[illegible]VSMFF[illegible]GHEWEVVHFLK[illegible]GWKIRKKYFLMKIKNQ[illegible]KERLVLSW 180
Db    121 PNNY[illegible]ANYTE[illegible]AL[illegible]VSMFF[illegible]GHEWEVVHFLK[illegible]GWKIRKKYFLMKIKNQ[illegible]KERLVLSW 180

Qy    181 ALLGPDKY[illegible]SDK[illegible]PSCLPPYIYEVIFATANESSALLIRMPNEKGILKDLIYK 240
Db    181 ALLGPDKYLSDK[illegible]PSCLPPYIYEVIFATANESSALLIRMPNEKGILKDLIYK 240

Qy    241 AKPKDPPLKKY[illegible]NPKK[illegible]LIKTY[illegible]VLKPLHDKGPFY[illegible]HLHASNVMLDGDT 300
Db    241 AKPKDPPLKKY[illegible]NPKK[illegible]LIKTY[illegible]VLKPLHDKGPFY[illegible]HLHASNVMLDGDT 300

Qy    301 [illegible]LENSLL[illegible]PSFYRSYFSQFPKINTLESVDVHCFGHLLYEMTYGRPPDSVPVDSFP 360
Db    301 [illegible]LENSLL[illegible]PSFYRSYFSQFPKINTLESVDVHCFGHLLYEMTYGRPPDSVPVDSFP 360

Qy    361 [illegible]PAPSMAVVAV[illegible]LKEALR 420
Db    361 PAPSMAVVAV[illegible]LKEALR 420

Qy    421 IAKECIEKELHEQKQIHQHRRLIFAQSHH 450
Db    421 IAKECIEKELHEQKQIHQHRRLIFAQSHH 450


RESULT 5
Q95RK3
ID   Q95RK3      PRELIMINARY;      PRT;   450 AA.
AC   Q95RK3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   LD22[illegible]6P
GN   CG8726.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID 7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN Y, CN BW SP;
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA   Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA   Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
RA   Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY061314; AAL28862.1; -.
SQ   SEQUENCE   450 AA;  50748 MW;  [illegible]BAB[illegible] CRC64;

  Query Match             25.3%;  Score [illegible];  DB [illegible];  Length 450;
  Best Local Similarity   40.2%;  Pred. No. 1.[illegible]-54;
  Matches  176;  Conservative   80;  Mismatches  1[illegible];  Indels   45;  Gaps   [illegible];

Qy     11 KVLLDDTVPLIAAIEASQSLQSHIEYIIRV[illegible]GISVENSW[illegible]IVKRYSDFD[illegible]LNNSLQIAG 70
Db     11 KLI[illegible]IQALS[illegible]ITAVQEVAGHIE[illegible]VWK[illegible]ASNENYWIV[illegible]KSLRVS[illegible] 70

Qy     71 LSLPLPPKKL[illegible]NMD[illegible]IAER[illegible]NY[illegible]ANYTE 130
Db     71 IELPLPRKKI[illegible]NMK[illegible]IAKKE[illegible]AKRPV[illegible]Y[illegible]HD 130

Qy    131 IALQQVSMFFRSEPKWEVVHFLK[illegible]KKE 175
Db    131 HAVQNAML[illegible]LRND[illegible]TWSL[illegible]KV[illegible]IVESGSQIHQ 188

Qy    176 ---------------------------[illegible]VLSWADLGPDKY[illegible]SDKDFQCL[illegible]KLLPSCLHPYI 209
Db    189 SKHFAACSSNGSCHSIDACTL[illegible] 248

Qy    210 YRVTFATANE[illegible]ALLIRMPNEK[illegible]IKTY 268
Db    249 EPVLLAAHTENGCLVIRKPHKHGTLK[illegible]MAANPKNT[illegible]NPKGRTALSMKQVATY 308

Qy    269 [illegible]KFLHDKGPFYGHLHASNVM[illegible]YFSQFPKIN 328
Db    309 GKQILEALIFLHSKGYAYGHLHSGN[illegible]GVFAFYEPEEMQHSKIH 368

Qy    329 TLESVDVHCFGHLLYEMTYGRPPDSVPVDSFPLAPSMAVVAVLESILSCEACKNGMPTTS 388
Db    369 AIETIDVYCFGHVLFEMAMGYPLQESVVRQ[illegible]LESILSKEACKAGLPILF 427

Qy    389 RLLQMPLFSDVLLTTSEK 406
Db    428 QLLGHRFFLQYASTESRR 445
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RESULT 6
Q9V344
ID   Q9V344       PRELIMINARY;      PRT;   563 AA.
AC   Q9V344;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CG8726 PROTEIN.
GN   CG8726.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003830; AAF59158.1; -.
DR   FlyBase; FBgn0033244; CG8726.
DR   InterPro; IPR000719; Euk_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Transferase.
SQ   SEQUENCE   563 AA;  62523 MW;  2517DC20C6671AEF CRC64;

  Query Match             23.1%;  Score 874;  DB 5;  Length 563;
  Best Local Similarity   30.2%;  Pred. No. 4.4e-54;
  Matches  [illegible];  Conservative   90;  Mismatches  188;  Indels   84;  Gaps   11;

Qy         84 MQREEIAERQK[illegible]NYLNV[illegible]NHLLSN[illegible]VKEF[illegible]NNYSANY[illegible]QVLMI[illegible] 143
Db          1 MEEEEIAEEKLA[illegible]EYINAVIMNE[illegible]AKSEVI[illegible]GHEHAV[illegible]NAME[illegible] [illegible]

Qy        144 PEWLVVEPLKE[illegible]GWRLEKKE[illegible]MLE[illegible]KN[illegible]PER----  [illegible]            175
Db         61 LIWSLGGSMGA[illegible]GWRLRKK[illegible]---KVI[illegible]SNE[illegible]VES[illegible]SQ[illegible]HQSERRFAAGSSNGSG 118

Qy        176               LVLSWAL[illegible]EKYL[illegible]KE[illegible]LHPY[illegible]YEVLLAIANE[illegible]A 222
Db        119 HSIDACTLDDPGSEVVAEWLEYGPDKFIDEKE[illegible]MKSLMCLQHPHIEPVLLAAHIENG[illegible] 178

Qy        223 [illegible] 281
Db        179 [illegible] 238

Qy        282 KGFPYGHLHASNVMLDGDT[illegible]RLLDLENSL[illegible]SPYRSYF[illegible]FRKINILESVDVHCPGHL 341
Db        239 KGYAYGHLHSGNIVIVD[illegible]VKLLDIENLL[illegible]VEAYKF[illegible]HSKIHA[illegible]VY[illegible]GHV 298

Qy        342 LYEMIY[illegible]EF[illegible]HEA[illegible]ENGMPLISRL[illegible]MPLESPVLL 401
Db        299 LFEMAMGYP[illegible]QESVVKQ[illegible]ALK[illegible]LESLLSKEA[illegible]EAGLPLLEQLLGHRE[illegible]QYAS 357

Qy        402 TTS-----  EEPQF[illegible]KRIAKE[illegible]RKQIHQHRK[illegible]KAQSHHGSEE 454
Db        358 TESAGAAANAEEP[illegible]NAE[illegible]NE[illegible]VKN[illegible]KRIVEVQPLMSSEE 417

Qy        455 EKKKKKILAKKKSKKSALENS   EEHSARYSNSNNSGSGASSPPT---------S 498
Db        418 EEKE[illegible]AELLHE[illegible]SKLE[illegible]INNG[illegible]VAATAAAAS[illegible]SSTIVVCEL[illegible]NKS 477

Qy        499 PSSPTPPSI-SGTSALPPPPPP--------PPPPAAPLPPASTEVPAQLSSQAVNG- 545
Db        478 DSIPEEPPIIAGIKSPPLPPGPHGSIYQQELPSIGAPVERQSS-TENMLSEDAEGGDG 536

Qy        546 --MSPGALLSS[illegible]QNPQECIT[illegible]EAKTCD 570
Db        537 DEPTRSALLESICKPNRGSLEEVRGND 563

RESULT 7
O61564
ID   O61564       PRELIMINARY;      PRT;   515 AA.
AC   O61564;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   SLOB (FRAGMENT).
GN   SLOB OR CG6772.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CANTON S;
RA   Schopperle W.M., Holmqvist M.H., Zhou Y., Wang J., Wang Z.,
RA   Griffith L.C., Keselman I., Dagan D., Levitan I.B.;
RL   Neuron 0:0-0(1998).
DR   EMBL; AF051162; AAC06289.1; -.
DR   FlyBase; FBgn0024290; Slob.
FT   NON_TER    515    515
SQ   SEQUENCE   515 AA;  57825 MW;  2189583D9D874FE5 CRC64;

  Query Match             13.1%;  Score 492.5;  DB 5;  Length 515;
  Best Local Similarity   30.3%;  Pred. No. 6.8e-29;
  Matches  122;  Conservative   58;  Mismatches  125;  Indels   97;  Gaps   13;

Qy        145 EWLVVEPLK[illegible]GWRLEKKE[illegible]MLE[illegible]KN[illegible]PER[illegible]---  -   VLSWAL[illegible]EKYL[illegible]KE[illegible] 195
Db        174 KYLV[illegible]AH[illegible]GKHGKNW[illegible]AV[illegible]VA[illegible]NECAR     E 229

Qy        196 [illegible] 251
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Db    2[illegible] [illegible]YKAQWNEPWAKKY 289

Qy    252 [illegible]NPKKIQ[illegible]KIY[illegible]YGHLHASNVMLDGDICKLLDLENSL 310
Db    290 [illegible]TEKENGL[illegible]VSQVQFLGEQIIEA[illegible]KFE[illegible]NVILQNGAAELSGLENGL 347

Qy    311 IGLPSFYRSYIFSQFKKINILESVIDVHCFGHLLYEMTYCRIPDSVPVDSFPPAPSMAVV-- 368
Db    348 [illegible]GLSSFINAVMWS[illegible]VTF[illegible]ENVF[illegible]V[illegible]GHL[illegible]YEM[illegible]  [illegible]PKFCMKVLEM 39[illegible]

Qy    369 -----------AVLEST-LSCEACKNGMP[illegible]ISF[illegible]QMHLFSDVLL[illegible]ISEKPQEKIPIK 414
Db    400 ELQHYPQIGQTRKQILEILGLIFFEPPSGVCPSVELLVICLLERSIDLRELRGPCF---ST 456

Qy    415 LKEALF[illegible]AKE[illegible]LEKEL[illegible]IEE[illegible]Q[illegible] [illegible]KKEK[illegible]LAKKE[illegible]KK[illegible]ALEN 474
Db    457 IKPSL---------------- ---- ---- ---SRSTLNLLQAVKKRQCA--- 478

Qy    475 SEEHSAKYSN[illegible]NNSG[illegible]CAS[illegible]PL[illegible]SP[illegible]PIPP[illegible]S[illegible]ISALPP[illegible] 516
Db    479 ---------SLGHSLSEANSPCTPPSTPHDRRT---GVLPAP 508


RESULT    8
Q9VL24
ID    Q9VL24       PRELIMINARY;       PRT;   515 AA.
AC    Q9VL24;
DT    01-MAY-2000 (TrEMBLrel. 13, Created)
DT    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT    01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE    SLOB PROTEIN.
GN    SLOB OR CG6772.
OS    Drosophila melanogaster (Fruit fly).
OC    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC    Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC    Ephydroidea; Drosophilidae; Drosophila.
OX    NCBI_TaxID=7227;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    STRAIN=BERKELEY;
RX    MEDLINE=20196006; PubMed=10731132;
RA    Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA    Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA    George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA    Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA    Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA    Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA    Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA    Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA    Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA    Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA    Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA    Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA    de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA    Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA    Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA    Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA    Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA    Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA    Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA    Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA    Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA    Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA    Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA    Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA    Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA    Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA    Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA    Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA    Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA    Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA    Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA    Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA    Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA    Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA    Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA    Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT    "The genome sequence of Drosophila melanogaster.";
RL    Science 287:2185-2195(2000).
DR    EMBL; AE003618; AAF52534.1; -.
DR    FlyBase; FBgn0024290; Slob.
SQ    SEQUENCE   515 AA;  57[illegible] MW;  [illegible] CRC64;

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  Best Local Similarity   30.3%;  Pred. No. [illegible];
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Db    174 KYEVIAHLDEIGSRHGKNWFLVTDASVRIDKLQ[illegible]LLFLFPICVAKEDLFPNETAK- -E 229

Qy    196 [illegible]LIKLLPSCLHPYIYKVT     FAIANK[illegible]ALL[illegible]MENE[illegible]LEL[illegible]YKAKPFDKFLKKY 251
Db    230 ILMELLGSLHHPYIYPVLDLGFLENSSYNYACLVIPFN[illegible]GSLKELLYKAQWNEPWAKKY 289

Qy    252 [illegible]NPKKIQGLFIQQIKIYGHQIIEV[illegible]K[illegible]KG[illegible]Y[illegible]HLASNVMLDGDICKLLDLENSL 310
Db    290 -TEKENGLPVSQVQFLGEQIIEA[illegible]KFE[illegible]NVILQNGAAELSGLENGL 347

Qy    311 IGLPS[illegible]YRSYI[illegible]SQFKKINILESVIDVH[illegible]GHLLYEM[illegible]YCRI[illegible]DSVPVD[illegible]PPAPSMAVV   368
Db    348 IGLSSFINAVMWS[illegible]VTF[illegible]ENVF[illegible]V[illegible]GHLLYEM[illegible]     [illegible]PKFCMKVLEM 399

Qy    369 ------------AVLEST-LSCEACKNGMPI[illegible]SF[illegible]QMHLFSDVLL[illegible]ISEKPQEKIPIK 414
Db    400 ELQHYPQIGQTRKQILEILGLIFFEPPSGVCPSVELLVICLLERSIDLRELRGPCF---ST 456

Qy    415 LKEALFKAKE[illegible]LEKEL[illegible]IE[illegible]Q[illegible] [illegible]KKEK[illegible]ALEN 474
Db    457 IKPSL---------------------- ---- ------SRSTLNLLQAVKKRQCA--- 478

Qy    475 SEEHSAKYSN[illegible]NNSGGCAS[illegible]PL[illegible]SP[illegible]PIPP[illegible]S[illegible]ISALPP[illegible] 516
Db    479 ---------SLGHSLSEANSPCTPPSTPHDRRT---GVLPAP 508


RESULT    9
Q95SL3
ID    Q95SL3       PRELIMINARY;       PRT;   280 AA.
AC    Q95SL3;
DT    01-DEC-2001 (TrEMBLrel. 19, Created)
DT    01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT    01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE    GH16988P.
GN    SLOB.
OS    Drosophila melanogaster (Fruit fly).
OC    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC    Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC    Ephydroidea; Drosophilidae; Drosophila.
OX    NCBI_TaxID=7227;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    STRAIN=Y; CN BW SP;
RA    Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA    Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA    Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA    Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
RA    Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL    Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR    EMBL; AY060721; AAL28269.1; -.
SQ    SEQUENCE   280 AA;  31454 MW;  [illegible] CRC64;

  Query Match             11.9%;  Score [illegible]7;  DB 5;  Length 280;
  Best Local Similarity   31.8%;  Pred. No. [illegible];
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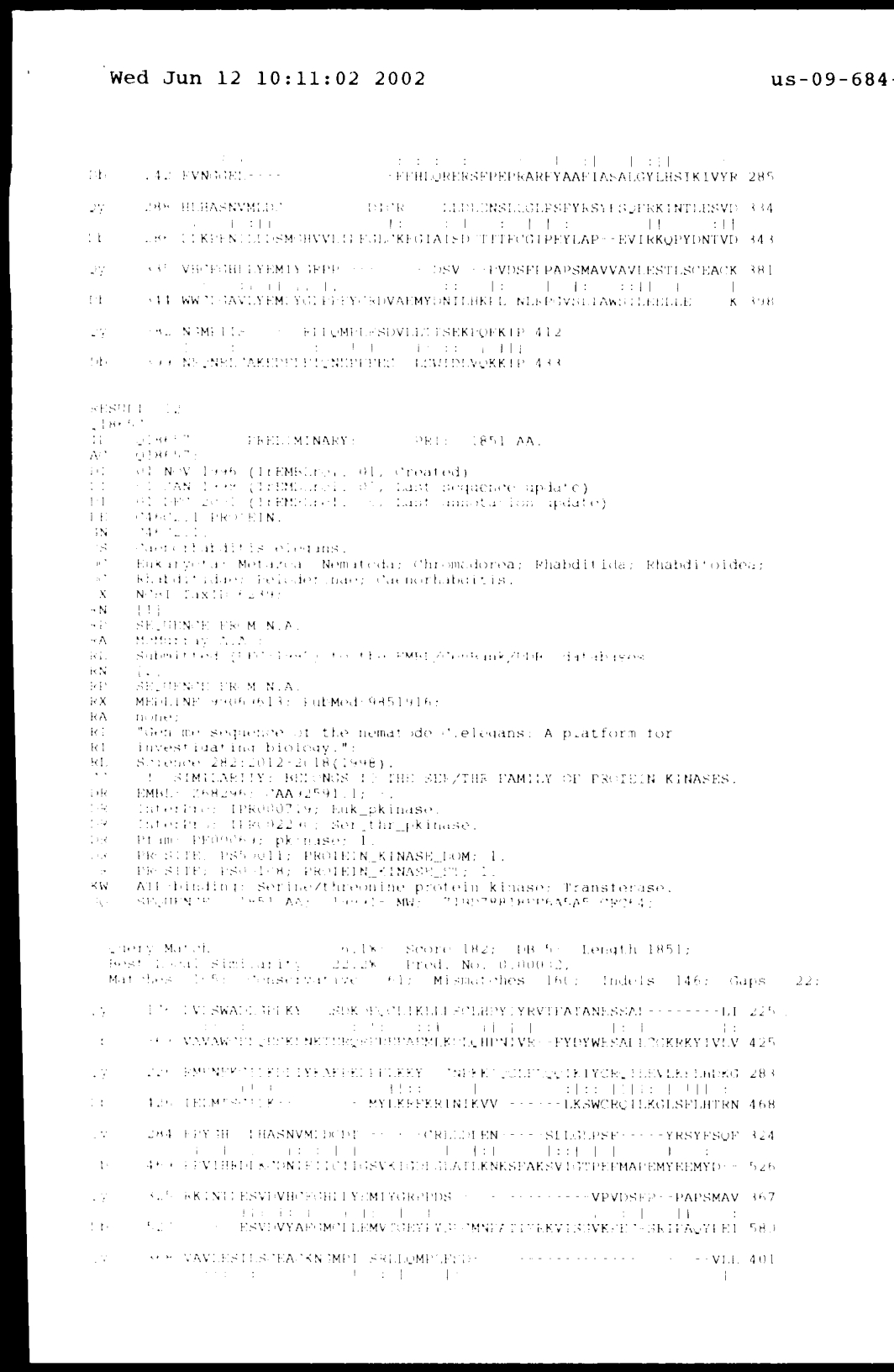

RESULT 13
Q96PY5
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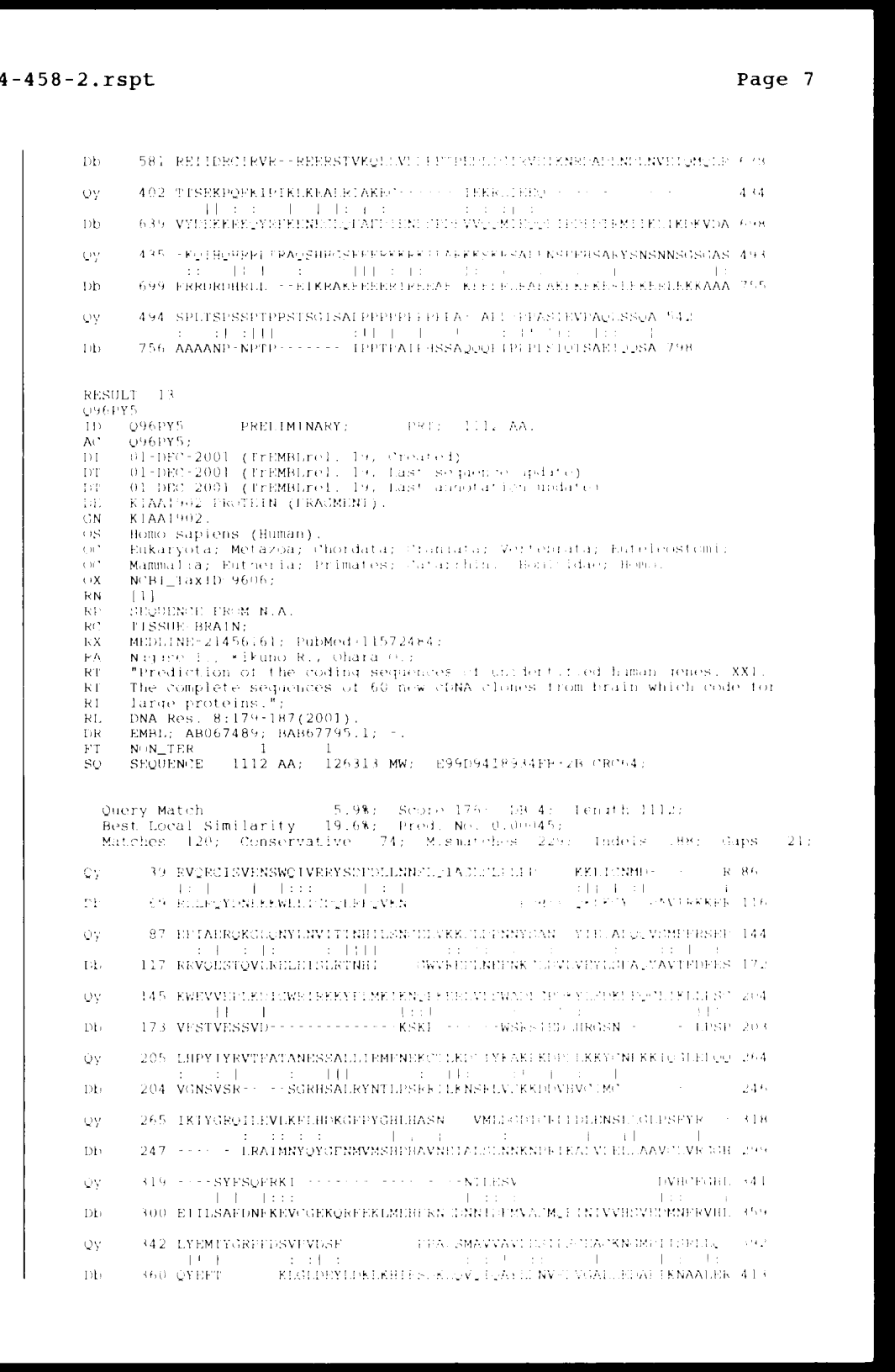
AC Q96PY5;
DT 01-DEC-2001 (TrEMBLrel. 16, Created)
DT 01-DEC-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 16, Last annotation update)
DE KIAA1902 PROTEIN (FRAGMENT).
GN KIAA1902.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=21456161; PubMed=11572484;
RA Nagase T., Kikuno R., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XXI.
RT The complete sequences of 60 new cDNA clones from brain which code for
RT large proteins.";
RL DNA Res. 8:179-187(2001).
DR EMBL; AB067489; BAB67795.1; -.
FT NON_TER 1 1
SQ SEQUENCE 1112 AA; 126313 MW; E99D9418934FF42B CRC64;

Query Match 5.9%; Score 175; DB 4; Length 1112;
Best Local Similarity 19.6%; Pred. No. 0.00045;
Matches 120; Conservative 74; Mismatches 229; Indels 188; Gaps 21;



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Qy        [illegible]       MP[illegible]ISEKPQEKIPIKLKEALPIAKE[illegible]IEKRLI  EEQKQIHQHRRL 443

Db    [illegible]4 VE[illegible]ENI[illegible]EKLQ[illegible]ENEAMGKIVELEKQLMQRNKELDVVREIYKDANIQVHILKKM 473

Qy    [illegible] [illegible]EA[illegible]                          KRSALENSEEHSARYSN 484

Db    [illegible] VKEKEEA[illegible]EKKIRLEEK[illegible]IKIQKKG[illegible]AILPVVASGILSMGSLVVAGNSV 533

Qy    [illegible] [illegible]NN[illegible]ASSPL[illegible]SSPIPPSISGISAL          PPPPPPPPPPAAP 526

Db    [illegible] [illegible]MGAA[illegible]PP[illegible]SSIPEIVQNGPVIPPMPPPPPPPPPPPPPPPPPPPP 593

Qy    [illegible] [illegible]PA[illegible]IEVPA [illegible]

Db    594 [illegible]PACEIVPA [illegible]4


RESULT 14
[illegible]
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AC   [illegible];
DT   [illegible] DEC 2001 (TrEMBLrel. 19, Created)
DT   [illegible] DEC 2001 (TrEMBLrel. 19, Last sequence update)
DT   [illegible] DEC 2001 (TrEMBLrel. 19, Last annotation update)
DE   SERINE/THREONINE PROTEIN KINASE (EC 2.7.1.37).
GN   PRKWNK1
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RA   [illegible] D.A.;
RL   [illegible] Department of INSERM U36, College de France, Paris,
RL   France.
DR   EMBL; A[illegible]; [illegible]; -.
KW   Kinase; Transferase.
SQ   SEQUENCE   1231 AA;  13[illegible]23 MW;  3B72881[illegible]8F433EE8 CRC64;

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  Best Local Similarity   22.0%;  Pred. No. 0.000098;
  Matches   [illegible];  Conservative   51;  Mismatches  128;  Indels  158;  Gaps   19;

Qy        178 LSWAD[illegible]PDKYLS[illegible]KE  [illegible]KLLP[illegible]LHPYIYRV   TFATANE[illegible]ALLIRMFNE 230

Db        [illegible] VAW[illegible]EK [illegible]EVLMEF[illegible]HPNIV[illegible]WE[illegible]VLK[illegible]V[illegible]IV[illegible]VT[illegible]LMI 246

Qy        231 K[illegible]AKR[illegible]KY[illegible]NPKKI[illegible]ILEVLKEIHDKGFPYGH - 288

Db        247 [illegible]LKIYL[illegible]KEMKP           EVLQRW[illegible]QILRGLHFLHS[illegible]VPPIL[illegible] 2[illegible]

Qy        289 LHASNVML[illegible]   [illegible]KLLDL      ENSLLGLPSF-----YRSYFSQFRKINLLF 331

Db        [illegible] [illegible]NVL[illegible]SVK[illegible]DLGLATLKRASFAKSVI[illegible]PEEMAPEMYEEKY[illegible]-------E 342

Qy        332 SV[illegible]EM                  [illegible]VPVDS[illegible]PPAPSMAVVAVL 371

Db        343 AVDVYAF[illegible]ILEMA[illegible]EY[illegible]QNAAQIYRKV[illegible]NSFH[illegible]VK[illegible]     [illegible]VKEI[illegible] 3[illegible]

Qy        [illegible] [illegible]MP[illegible]     VL[illegible]    [illegible]SEE[illegible]KIKEALR     42[illegible]

Db        3[illegible]8 E[illegible]  KNEKF[illegible]QDLLAHAFFKEEKGVHVELAEEDDGEKPGLKLWLRMEDARRGGR 45[illegible]

Qy        421                 IAKECIEKRLIEEQKQIHQHRRLIRAQSHIGSEEERKKRK 460

Db        4[illegible] EE[illegible]NLAIE[illegible]L[illegible]AAEEVAQEMVALGLVCEA     DYQPVARAVRERVAAIQRKREK 511

Qy        461 IIAFKKSK[illegible]ALENSEEHSARYSNGNNSGSMASSPLISPSSPIPPSISGISALPPPPPPP 520

Db        512 [illegible]       RKARE                   LEALPPEPGPP 528
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Qy        521 PP-PAAPLPPA 530

Db        529 PATVPMAPGPPS 540


RESULT 15
Q96J92
ID   Q96J92      PRELIMINARY;      PRT;  1243 AA.
AC   Q96J92;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPOTHETICAL 134.7 KDA PROTEIN.
GN   PRKWNK4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RX   MEDLINE=21390047; PubMed=11498583;
RA   Wilson F.H., Disse-Nicodeme S., Choate K.A., Ishikawa K.,
RA   Nelson-Williams C., Desitter I., Gunel M., Milford D.V., Lipkin G.W.,
RA   Achard J.-M., Feely M.P., Dussol B., Berland Y., Unwin R.J., Mayan H.,
RA   Simon D.B., Farfel Z., Jeunemaitre X., Lifton R.P.;
RT   "Human Hypertension Caused by Mutations in WNK Kinases.";
RL   Science 293:1107-1112(2001).
DR   EMBL; AF390018; AAK91995.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   1243 AA;  134730 MW;  BAC35F0098BA3391 CRC64;

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  Best Local Similarity   22.0%;  Pred. No. 0.00099;
  Matches   95;  Conservative   51;  Mismatches  128;  Indels  158;  Gaps   19;

Qy        178 LSWADL[illegible]PDKYLSDKE  [illegible]QCLIKLLPSCLHPYIYRV   TFATANESSALLIRMFNE 230

Db        200 VAWCELQTRK-LSRAERQRFSEEVEMLKGLQHPNIVRFYDSWKSVLRGQVCIVLVTELMT 258

Qy        231 K[illegible]KLLIYKAK[illegible]K[illegible]   VK[illegible]  [illegible]PYCH   288

Db        259 SGTLKTYLRRFREMKP          RVLQRWSRQILRGLHFLHSRVPPILHRD 302

Qy        289 LHASNVMLD[illegible]   CKLLDL         ENSLLGLPSF     YRSYFSQFRKINLLF 331

Db        303 LKCDNVF[illegible]SVK[illegible]ATLKRASFAKSVI[illegible]PEEMAPEMY[illegible]     E 354

Qy        332 SVDVHCPGHLLYEM-------------------TYCRPPDSVPVDSPPPAPSMAVVAVL 371

Db        355 AVDVYAF[illegible]ILEMA[illegible]EY[illegible]QNAAQIYRKV[illegible]     [illegible]VKEI 409

Qy        372 [illegible]MP[illegible]      V[illegible]     [illegible]EALR   420

Db        410 EQCIRTD--KNERFTIQDLLAHAFFREERGVHVELAEEDDGEKPGLKLWLRMEDARRGGR 467

Qy        421                 IAKECIEKRLIEEQKQIHQHRRLIRAQSHIGSEEERKKRK 460

Db        468 [illegible]VAKAV[illegible]AA[illegible]

Qy        461 [illegible]ALENSEE[illegible]   [illegible]SISGISALPPPPPPP 520

Db        524 [illegible]     RKARE                   LEALPPEPGPP 540

Qy        521 PP--PAAPLPPA 530

Db        541 PATVPMAPGPPS 552


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